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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu Jul 30 09:30:16 1998; MasPar time 4.32 Seconds 278.747 Million cell updates/sec OD:

Jular output not generated.

>US-08-938-548A-11 (1-33) from US08938548A.pep 256 1 QPLPDCCRQKTCSCRLYELLHGAGNHAAGILTL 33 Description: Perfect Score:

Sequence:

PAM 150 Gap 11 Scoring table:

120441 seqs, 36531193 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d Database:

Mean 30.310; Variance 51.743; scale 0.586 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	9.01e-01	1.84e+00	2.63e+00	2.63e+00	3.73e+00	5.28e+00	5.28e+00	7.44e+00	7.44e+00	7.44e+00	1.05e+01	1.05e+01	1.05e+01	1.46e+01	1.46e + 01	1.46e+01	1.46e+01	1.46e + 01	1.46e+01	1.46e+01	1.46e + 01	1.46e+01	1.46e + 01
Description	hypothetical protein	dystrophin homolog -	oct2 protein isoform	sperm_mitochondrial c	tetracycline-minocycl	Ig alpha chain C regi	Ig alpha chain C regi		gene D3 protein - mou	transcriptional regul	hypothetical protein	keratin KAP5.5 - shee	beta-fructofuranosida	Omega-aga-ivb (nmr, m	Omega-aga-ivb (nmr, 2	omega-agatoxin-ivb -	omega-agatoxin IVB -	omega-agatoxin III, 8	omega-agatoxin IIIA -	omega-agatoxin III, 8	cell division protein	pigment deposition co	agouti protein precur
£	S24303	A41130	860079	A37199	JN0800	AHRB	S09276	S11223	156329	B69764	C64314	146413	S33920	10MB	10MA	IAGG	A44664	B54252	A42335	A54252	B64052	A46298	137143
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Length	147	870	93	143	641	299	338	347	425	479	155	197	589	32	48	48	48	92	26	76	103	131	132
% Query Match	28.1	27.3	27.0	27.0	26.6	26.2	26.2	25.8	25.8	25.8	25.4	25.4	25.4	25.0	25.0	25.0	25.0	25.0	25.0	25.0	25.0	25.0	25.0
Score	72	70	69	69	89	29	29	99	99	99	65	65	65	64	64	64	64	64	64	64	64	64	64
Besult No.	, , ,	7	٣	4	Ŋ	ø	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23

1.46e+01 2.04e+01 2.04e+01 2.04e+01 2.04e+01 2.04e+01 2.04e+01 2.04e+01 2.04e+01 2.04e+01 2.04e+01 2.04e+01	2.846-01 2.846-01 2.846-01 3.946-01 3.936-01 3.936-01 3.936-01 3.936-01 3.936-01
hypothetical protein cysteine proteinase (hypothetical protein Ig alpha chain C regiamino acid transport angiotensin precursor tetracycline resistan tetracycline resistan tetracycline resistan hypothetical 17.9K primorsin haavy chain.	a at the a
B64835 S49175 H69619 S09271 B59479 A29978 S13142 A50633 A56779 JC5551 H0799	S47555 S29159 A43374 A336426 D54252 M428BC7 A428BC7 S32337 S64859 B43402
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0.0000000000000000000000000000000000000	44444666666 64444666666666666666666666
44EEEEEEE	61 61 61 61 61 61
	0 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6

ALIGNMENTS

S24303 #type complete hypothetical protein H19-3' - mouse #formal_name Mus musculus #common_name house mouse 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 10-Sep-1997	S2 S2 Po De Th Th Ule_ty ues -refer #1	tch 28.1%; Score 72; DB 2; Length 147; al Similarity 32.1%; Pred. No. 9 01e-01; 9; Conservative 9; Mismatches 10; Indels 0; Gaps 0; CCNONHYTTCLRNLLQGEAERTDGVNIL 93 :	TEX A41130 #type fragment dystrophin homolog - Pacific electric ray (fragment) ERNATE_NAMES 300k subsynaptic protein #formal_name Torpedo californica #common_name Pacific electric ray (3-dug-1992 #sequence_revision 03-dug-1992 #text_change 23-Jan-1998
RESULT 1 ENTRY TITLE ORGANISM	ACCESSIONS REFERENCE #authors #journal #title #accession ##cession ##fectus ##molecule ##molecule ##residues ##residues ##residues	Query Match Best Local Similarity Matches 9; Conserv Db 66 CCNQNHYTTCLRNLI	RESULT 2 ENTRY TITLE ALTERNATE_NAMES ORGANISM DATE ACCESSIONS REFERENCE #authors #Journal #title #corossion #accession #accession #accession #accession #anolecule_ ##residues

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##residues 1-347 ##label ZES
##cross-references EMBL:X53949; NID:g57791; PID:g57792
                                                                                                                                                                                                                                                                                                                                12 CSCRLYELLHGAG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156329
                                                                             CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##status
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#authors
#journal
#title
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SUMMARY
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                                       GENETICS
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#superfamily immunoglobulin C region; immunoglobulin homology
immunoglobulin
                                                           *superfamily immunoglobulin C region; immunoglobulin homology duplication; glycoprotein; heterotetramer; immunoglobulin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #journal Nucleic Acids Res. (1990) 18:5289
#title CDNA from rat cells with reconstitutive galactose-epimerase activity in E. coli.
#cross-references MUID:90384840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zeschnigk, M.; von Wilcken-Bergmann, B.; Starzinski-Powitz
 stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger
                                                                                                                              #domain immunoglobulin homology #label IGG1\
#domain immunoglobulin homology #label IGG2\
#binding_site carbohydrate (Asn) (covalent) #status
predicted
#length 299 #checksum 2361
                                                                                                                                                                                                                                                                                                                                                                                                                                            S09276 #type fragment
Ig alpha chain C region - rabbit (fragment)
#formal_name Oryctolagus cuniculus #common_name domestic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UDPglucose 4-epimerase (EC 5.1.3.2) - rat

UDPgalactose 4-epimerase

#formal_name Rattus norvegicus #common_name Norway rat

18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change

08-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 16-Aug-1996 S09276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Burnett, R.C.; Hanly, W.C.; Zhai, S.K.; Knight, K.L. EMBO J. (1989) 8:4041-4047
EMBO JA, Abeavy-chain gene family in rabbit: cloning and sequence analysis of 13 C-alpha genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #domain immunoglobulin homology #label IGG2 #length 338 #checksum 2169
                                                                                                                                                                                                                                                   Score 67; DB 1; Length 299;
Pred. No. 5.28e+00;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   not compared with conceptual translation
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Pred. No. 5.28e+00;
4; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         **status preliminary **molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 26.2%;
Local Similarity 50.0%;
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Best Local Similarity 50.0%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83 PFPDCCPANSCCTC 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:|||| ::| :|
2 PLPDCCRQKTC-SC 14
                                                                                                                                                                                                                                                                                                                                44 PFPDCCPANSCCTC 57
                                                                                                  plasma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S09276
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KEYWORDS
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#title
                                                                                                                  FEATURE
86-152
189-261
38,286
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ENTRY
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Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.;
Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.;
Bolothin, A.; Borchert, S.; Boriss, R.; Boursier, L.; Brans,
A.; Braun, M.; Brignell, S.C.; Bron, S.; Brouillet, S.;
Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
Choi, S.K.; Codani, J.J.; Connerton, I.F.; Cummings, N.J.;
Daniel, R.A.; Denizot, F.; Devine, K.M.; Duesterhoeft, A.;
Ehrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J.;
Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fulita,
M.; Fulida, Y.; Funa, S.; Galiszi, A.; Galleron, N.; Ghim,
S.Y.; Glaser, P.; Goffeau, A.; Golighily, E.J.; Grandi, G.;
Guiseppi, G.; Guy, B.J.; Haga, K.; Halech, J.; Harwood,
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A lipopolysaccharide-inducible macrophage gene (D3) is a member of an interferon-inducible gene cluster and is
                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156329 #type complete
gene D3 protein - mouse
#formal_name Mus sp. #common_name mouse
26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
28-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
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#superfamily Escherichia coli UDPglucose 4-epimerase;
UDPglucose 4-epimerase homology
                                                                                                                                    #domain UDPglucose 4-epimerase homology #label 8#length 347 #molecular-weight 38225 #checksum 6947
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#length 425 #molecular-weight 47046 #checksum 8487
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                                                                                                                                                                                                              Score 66; DB 2; Length 347; Pred. No. 7.44e+00; 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 66; DB 2; Length 425;
Pred. No. 7.44e+00;
10; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##residues 1-425 ##label RES
##cross-references GB:S62227; NID:9385702; PID:9385703
                                                                               galactose metabolism; isomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 PPCCEEPTAMCQ-SPILHSSSSASSNILS 205
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Best Local Similarity 53.8%;
Matches 7; Conservative
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Best Local Similarity 31.0%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                         261 CGCRIYNLGTGTG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##molecule_type mRNA
##residues 1-425
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Fauthors Yu, H.; Rosen, M.K.; Schreiber, S.L.
Fsubmission submitted to the Brookhaven Protein Data Bank, September 1993
Fcross-references PDB:10MB
FGRIT Resolution: not applicable
FROM Determination: NMR
#product beta-fructofuranosidase #status experimental #label SIG\ #label MAT\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #authors Yu, H.; Rosen, M.K.; Schreiber, S.L.
#submission submitted to the Brookhaven Protein Data Bank, September 1993
#scross-references PDB:10MA
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Omega-aga-ivb (nmr, 21 structures) - funnel-weaving spider
(Agelenopsis aperta)
                                                                                                   #binding_site carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                predicted\
    #binding_site phosphate (Thr) (covalent) #status
    predicted\
    #binding_site phosphate (Ser) (covalent) #status
    predicted
#length 589 #molecular-weight 63650 #checksum 1032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #disulfide_bonds
#length 35 #molecular-weight 3804 #checksum 7419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           LOMB #type complete
Omega-aga-ivb (nmr, minimized average struct
funnel-weaving spider (Agelenopsis aperta)
#formal_name Agelenopsis aperta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 25.0%; Score 64; DB 5; Length 48; Best Local Similarity 45.5%; Pred. No. 1.46e+01;
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Pred. No. 1.46e+01;
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A51322
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#region turn (type I
#disulfide_bonds\
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Best Local Similarity 45.5%;
Matches 5; Conservative
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                                                            36,42,170,188,211,
254,259,318,322,
388,463,518,527
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10-13
1-17
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24-589
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REFERENCE
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REFERENCE
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24-31
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4-20
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19-36
27-34
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ENTRY
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Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Db 19 CCRGRPCRCSM 29

||| : | | :
Qy 6 CCRQRTCSCRL 16

Search completed: Thu Jul 30 09:30:35 1998
Job time : 19 secs.
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Thu Jul 30 09:32:10 1998; MasPar time 1.21 Seconds 159.253 Million cell updates/sec abular output not generated. : uo

>US-08-938-548A-11 (1-33) from US08938548A.pep 256 1 QPLPDCCRQKTCSCRLXELLHGAGNHAAGILTL 33 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

63816 seqs, 5850866 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

a-issued 1:5_COMB 2:PCT9_COMB 3:backfiles Database:

Mean 21.451; Variance 82.349; scale 0.260 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.
Description
. А
Length DB
Query
Score
ult No.

27. 22.3 790 1 US-08-363- Sequence 20, Applicatio 1.24e+02 57 22.3 1184 1 US-08-446- Sequence 20, Applicati 1.24e+02 57 22.3 1187 1 US-08-346- Sequence 20, Applicati 1.24e+02 57 22.3 1187 1 US-08-037- Sequence 13, Applicatio 1.24e+02 57 22.3 1187 1 US-08-097- Sequence 13, Applicatio 1.24e+02 28 1187 2 PCT-US95-1 Sequence 49, Applicatio 1.24e+02 28 1187 2 PCT-US95-1 Sequence 49, Applicatio 1.24e+02 28 1187 2 PCT-US95-1 Sequence 49, Applicatio 1.50e+02 28 1187 2 PCT-US95-1 Sequence 49, Applicatio 1.50e+02 28 117308-12 Patent No. 5177308-1 1.50e+02 28 1 US-08-161- Sequence 1, Applicatio 1.50e+02 28 1 US-08-161- Sequence 1, Applicatio 1.50e+02 28 1 US-08-485- Sequence 13, Applicatio 1.50e+02 28 1 US-08-485- Sequence 13, Applicatio 1.50e+02 28 1 US-08-485- Sequence 3, Applicatio 1.50e+02 28 2 US-08-485- Sequence 7, Applicatio 1.50e+02 28 2 US-08-485- Sequence 7, Applicatio 1.50e+02 28 2 US-08-452- Sequence 2, Applicatio 1.50e+02 20 20 20 20 20 20 20 20 20 20 20 20 2	T 1 19-249-322A-40 STANDARD; PRT; 39 AA. XXXXXXX XXXXXXX Sequence 40, Application US/08249322A SEGREAL INCRAMITION: Water Waterifield, Michael; Marchioni, Mark; APPLICANT: Minghettl, Luisa; Waterifield, Michael; Marchioni, Mark; APPLICANTON: Preparation and Use CORRESPONDENCE ADDRESS: ADDRESSEE Relie 6 Lynch STREE: New York City CONFUTER READABLE FORM: MEDUM TYPE: Diskette, 5.25 inch, 360 kb storage CONFUTER READABLE FORM: MEDUM TYPE: Diskette, 5.25 inch, 360 kb storage CONFUTER READABLE FORM: CONFUTER READABLE FORM: MEDUM TYPE: Diskette, 5.25 inch, 360 kb storage CONFUTER READABLE FORM: CONFUTER READABLE FORM: MEDUM TYPE: Diskette, 5.25 inch, 360 kb storage CONFUTER READABLE: POWN NUMBER: US/0924, 332A FILING DATE: 23-04710N DATA: APPLICATION NUMBER: US/0925, 339 PRIOR APPLICATION DATA: APPLICATION NUMBER: US/0921, 389 PRIOR APPLICATION NUMBER: US/0921, 389
20000000000000000000000000000000000000	RESULT 1 TID 08-08- XXX XXXXXX XXXXXXX XXXXXXX XXXXXXX XXXXX
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PRIOR APPLICATION DATA
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ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
ZIF: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 40, Application PC/TUS9405083C
GENERAL INFORMATION:
APPLICANT: Robert Sklar, Mark Marchionni,
APPLICANT: David I. Gwynne
TITLE OF INVENTION: METHODS FOR ALTERING
TITLE OF INVENTION: MUSCLE CONDITION
NUMBER OF SEQUENCES: 185
FILING DATE: 03-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/907,138
FILING DATE: 30-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/863,703
FILING DATE: 03-APRL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.K. 91 07566.3
FILING DATE: 10-APRIL-1991
ATGNEEZ AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                          NAME: Hanson, Norman D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5250.5
TELECOMUNICATION INFORMATION:
TELECHONE: (212) 689-9200
TELERAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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SOFTWARE: WOrdperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05083C
FILING DATE: 06-MAY-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,204
FILING DATE: 08-YAR-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/059,022
FILING DATE: 06-May-93
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 40, Application PC/TUS9405083C
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Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25.8%;
ilarity 70.0%;
Conservative
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SEQUENCE 39 AA; 3760 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM
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Best Local Similarity
Matches 7; Conser
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Patent No. 560632
GENERAL INFORMATION:
APPLICANT: Goodearl, Andrew; Stroobant, Paul;
APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
APPLICANT: Chen, Maio Su; Hiles, Ian
TITLE OF INVENTION: Glial Mitogenic Factors, Their
TITLE OF INVENTION: Preparation and Use
NUMBER OF SEQUENCES: 184
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39 AA.
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE-DOCKET NUMBER: 04585/028WO1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: 200154
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                            Score 66; DB 2; L
Pred. No. 2.23e+01;
1; Mismatches 1
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COMPUTER: 1BM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,569
FILING DATE: 06-UN-1995
CLASSIFICATION: 30
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/036,555
FILING DATE: 24-MAR-1993
APPLICATION NUMBER: 07/965,173
FILING DATE: 23-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/965,173
FILING DATE: 23-OCT-1992
APPLICATION NUMBER: 07/965,173
FILING DATE: 03-OCT-1992
APPLICATION NUMBER: 07/965,173
FILING DATE: 03-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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FILING DATE: 03-SEP-1992
PRIOR APPLICATION DATA: 07/907,138
APPLICATION NUMBER: 07/907,138
FILING DATE: 30-JUN-1992
PRIOR APPLICATION DATA:
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03-APRIL-1992
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                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
CE 39 AA; 3760 MW; 6521 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Glial Mil
TITLE OF INVENTION: Glial Mil
TITLE OF INVENTION: Preparat:
NUMBER OF SEQUENCES: 184
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                            25.8%;
70.0%;
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Best Local Similarity 70.00.
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SEQUENCE
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                                                                                                                                                                                                                                                                                          Sequence 9, Application US/08620717A
Patent No. 5670365
GENERAL INFORMATION:
APPLICANT: Feitelson, Jerald S.
TITLE OF INVENTION: Identification of, and Uses For, Nematicidal
TITLE OF INVENTION: Bacillus thuringiensis Genes, Toxins, and Isolates
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Salivanchik & Salivanchik
GENERAL IN IN IN INC.
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                                                                                                                         Score 64; DB 1; Length 1167;
Pred. No. 3.29e+01;
3; Mismatches 3; Indels
                                                                                                                                                                                                                      1168 AA
                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1 STATE: Florida
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/540,104
FILING DATE: 06-0CT-1995
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA94.C1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 10FORMATION:
TELECHONE: (352) 375-6100
INFORMATION FOR SEQ ID NO: 9:
REFERENCE/DOCKET NUMBER: MA48DD2.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904, 375-8100
TELEPAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1167 amino acids
                                                                         STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 1167 AA; 131657 MW; 7095219 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/620,717A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SYSTEMARE: Patentin
                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                            Sequence 9, Application US/08620717A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1168 amino acids
                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                         Query Match
Best Local Similarity 45.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                  TYPE: amino acid
                                                                                                                                                              873 PNCCKPAACQC 883
                                                                                                                                                                        |:||: :| |
4 PDCCRQKTCSC 14
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US-08-620-717A-9
                                                                                                       SEQUENCE
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Gaps
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Patent No. 5502166
GENERAL INFORMATION:
APPLICANT: Masayoshi MISHINA
APPLICANT: Masayoshi MISHINA
TITLE OF INVENTION: NOVEL PROTEINS AND GENES CODING THE SAME
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                            ö
                                                                           Length 1168;
                                                                        Score 64; DB 1; Length 1168 Pred. No. 3.29e+01; 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 5214, Nishlohata Residence 1-107
STREET: 5214, Nishlohata-machi
CITY: Niigata-shi
STATE: Niigata-ken
COUNTRY: JAPAN
ZIP: 951
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: MS-DOS v.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 to 1464
CE 1464 AA; 165489 MW; 11224000 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE TYPE: cerebellum
PUBLICATION INFORMATION:
AUTHORS: Masayoshi MISHINA
TITLE: NOVEL PROTEINS AND GENES CODING THE SAME
                                                                                                                                                                                                                                                                                                                                  1464 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 39563/1992
APPLICATION NUMBER: JP 39563/1992
APPLICATION NUMBER: JP 173155/1992
APPLICATION NUMBER: JP 173155/1992
APPLICATION NUMBER: JP 215017/1992
APPLICATION NUMBER: JP 303878/1992
APPLICATION NUMBER: JP 303878/1992
ATTORNEY/AGENT INFORMATION:
NAME: Hamburg, C.Bruce
REGISTRATION NUMBER: Z-3389
REFERENCE/DOCKET NUMBER: F-4551
TELECOMMUNICATION INFORMATION:
INDIVIDUAL ISOLATE: 167p
SEQUENCE 1168 AA; 131542 MW; 7175894 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: MS-DOS v.5
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/026,138E
FILING DATE: 26-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08026138E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1464 amino acids
TYPE: amino acid
STRANDEDNESS: Single strand
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (212) 986-2340
TELEFAX: (212) 953-7733
INFORMATION FOR SEO ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                      Query Match 25.0%;
Best Local Similarity 45.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: mouse
                                                                                                                                                                           873 PNCCKPAACQC 883
                                                                                                                                                                                                                            4 PDCCROKTCSC 14
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XXXXX

RESULT ID US

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5; Indels
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                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue N.W., Suite 1000
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 61; DB 1; L
Pred. No. 5.85e+01;
                                                                                                                                                                                  APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: McIntosh, J. Michael
APPLICANT: Santos, Ameurfina D.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24260-104763
                                                                                                                                                                                                                                                                                                                                                                                             CITY: Washington
STATE: DC
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,800
FILING DATE: 19-OCT-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INPORMATION:
NAME: Ihnen, Jeffrey L.
NAME: Ihnen, Jeffrey L.
NAME: Ihnen, Jeffrey L.
NAME: Ihnen, Jeffrey L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 51, Application US/08233788A
Patent No. 5635617
GENERAL INFORMATION:
APPLICANT: Dozan, James L.
                                                                                                                     Sequence 23, Application US/08137800 Patent No. 5514774 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 51, Application US/08233788A
                                                                                Sequence 23, Application US/08137800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NISM: Conus ochroleucus
42 AA; 4618 MW; 9505 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION
TELEPHONE: 202-962-4810
TELEFRA: 202-962-830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 42 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IUPOLGGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 PLP-DCCRQKTCSCRLYEL 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
23.8%;
Best Local Similarity 47.4%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2
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ID US-08-233-788A-51

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DT

XX

DE

Sequence 51, Applica

XX

CC

Sequence 51, Applic

CC

Patent No. 5635617

CC

APPLICANT: Doru
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XXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTE: 20003
COMPUTE: Floppy disk
APPLICATION NUMBER: US/08/477,383
FLING DATE: 19-OCT-1993
PRIOR APPLICATION NUMBER: US 08/084,848
FILING DATE: 29-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: INDO. JEFFERDENCE/DOCKET NUMBER: 28,957
REGISTENCE/DOCKET NUMBER: 28,957
REGISTENCE/DOCKET NUMBER: 28,957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
                                       42 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 AA.
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Pred. No. 5.85e+01;
3; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                Conotoxin Peptides 59
                                                                                                                                                                                                    Sequence 23, Application US/08477383
Patent No. 5589340
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M. APPLICANT: Cruz, Lourdes J. APPLICANT: Hillyard, David R. APPLICANT: Macintosh, J. Michael APPLICANT: Santos, Ameurfino S. TITLE OF INVENTION: Conotoxin Pepti NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
ORGANISM: Conus ochroleucus
JENCE 42 AA; 4618 MW; 9505 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 PLP-DCCRQKTCSCRLYEL 19
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Best Local Similarity 47.4%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 20005
                   JT 12
US-08-477-383-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
ID US-08-137-800-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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Gaps

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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu Jul 30 09:29:43 1998; MasPar time 7.52 Seconds 67.356 Million cell updates/sec ular output not generated. Run on:

>US-08-938-548A-11 (1-33) from US08938548A.pep Description: Perfect Score: Title:

1 QPLPDCCRQKTCSCRLYELLHGAGNHAAGILTL 33 256 Sequence:

Scoring table:

PAM 150 Gap 11

124785 segs, 15338987 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-geneseg31-2
lipart1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part18 21:part20 21:part21 22:part22 23:part23 24:part27

Mean 22.991; Variance 84.736; scale 0.271 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STAMMARTES

	& 0.1910					
Score	Match	Match Length DB	ВВ	QI	Description	Pred. No.
77	30.1	363	23	W12414	Porcine complement in	6.26e+00
75	29.3	373	18	R98461	Murine ICE-ced-3 homo	9.46e+00
75	29.3	373	13	R66767	Murine interleukin-1	9.46e+00
69	27.0	329	56	W29877	Lysophosphatidic acid	3.20e+01
99	25.8	102	Н	P95679	Xenopus Vql protein f	5.80e+01
99	25.8	348	20	W01619	Human uridine diphosp	5.80e+01
65	25.4	78	S	P20020	Sequence of a foot an	7.06e+01
64	25.0	45	23	W10106	Human agout1 signall1	8.59e+01
64	25.0	45	23	W10105	Murine agout1 signall	8.59e+01
64	25.0	48	σ	R45611	AG1 toxin.	8.59e+01
64	25.0	48	1	R60293	Calcium channel inhib	8.59e+01
64	25.0	48	œ	R44209	A. aperta venom fract	8.59e+01
64	25.0	130	23	W10102	Human agouti signalli	8.59e+01
64	25.0	131	23	W10101	Murine agouti signall	8.59e+01
64	25.0	1167	23	W31504	Nematode toxin 167P p	8.59e+01
64	25.0	1167	20	W10653	Bacillus thuringiensi	8.59e+01
64	25.0	1168	23	W16326	Nematocidal toxin 167	8.59e+01
62	24.2	34	9	R55088	Tarantula spider veno	1.27e+02
62	24.2	1464	10	R55529	Human NMDA R2A recept	1.27e+02
	, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		200 200 200 200 200 200 200 200 200 200	20011 20022 2013 2013 2013 2013 2013 201	30.1 363 23 29.3 373 18 29.3 373 18 29.3 373 18 25.0 329 26 25.8 348 20 25.0 45 23 25.0 48 11 25.0 48 11 25.0 130 23 25.0 1167 27 25.0 1167 27 25.0 1167 27 25.0 1167 27 25.0 1167 27 25.0 1168 23 25.0 1167 27 25.0 1167 27	30.1 363 23 W11414 29.3 373 18 R98461 29.3 373 18 R69461 25.8 10.2 18 P95679 25.8 10.2 1 P95679 25.0 45 23 W10106 25.0 45 23 W101010 25.0 48 18 R6429 25.0 130 23 W10101 25.0 130 22 1167 20 W1053 25.0 1167 20 W1053 25.0 1167 20 W1053 25.0 1167 20 W1053 25.0 1167 20 W1053 24.2 1464 10 R55529

1.27e+02 1.27e+02 1.27e+02 1.27e+02 1.53e+02 1.5	77
Human N-methyl-D-aspa Human excitatory amin Glutamic acid recepto Rat NMDA receptor sub A-lineage conotoxin p Predatory cone snail Salmonella enteritidi Human membrane antige TctA sequence. Human by protein asso Gyn d allergen Bl. Cherry polyphenol oxi E. coli DNA polymeras DNA polymerase III ho APP-HCV-E2 fusion pro Spider venom peptide N-terminal sequence o Funnel-web spider ven Connexin-32. Sequence of viper ven Sequence of viper ven Ovine FSH beta subuni	~
R66039 R80970 R41054 R441054 R12745 W1274890 W27333 W27559 W31950 W31950 W31671 R40115 R40115 R42948	W31948 W23594
1188 12222330338 20222333033 20222333 20333 20333 20333 20333	27
114664 114664 12664 126644 12664 126644 1266	2186 3788
444448888888888888888888888888888888888	22.7
	20.00
0110840900000000000000000000000000000000	4 4 5

ALIGNMENTS

DNA encoding porcine complement inhibitor - useful in porcine organ transplant to humans claim 5; page 12-14; 20pp; Japanese.

This protein is a porcine complement inhibitor encoded by pMCPCDNA (T61098). The DNA is useful for large scale production of recombinant porcine complement inhibitor, which is useful for porcine organ transplantation into humans. The DNA clone pMCPCDNA is also useful in the analysis of the promoter region of porcine complement inhibitor. W12414;
24-SEP-1997 (first entry)
Porcine complement inhibitor.
porcine; plg; complement; inhibitor; organ transplantation; analysis; promoter. χ; Toyomura 09-JAN-1997. 19-JUN-1996; JO1704. 20-JUN-1995; JP-178254. (NIME-) NIPPON MEAT PACKERS INC. (NIMA-) NIPPON HAM KK. (NIHA-) NIPPON HAM KK. NUTAKAMI H. SALIGENISS T, TOYOMUR W12414 standard; Protein; 363 AA. 363 AA; N-PSDB; T61098. Sus scrofa. WO9700951-A1. Sequence

ä Score 77; DB 23; Length 363; Pred. No. 6.26e+00; 7; Mismatches 9; Indels Query Match 30.1%; Best Local Similarity 39.3%; Matches 11; Conservative

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Gaps

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LT 2 R08461 standard; Protein; 373 AA. R08452-1996 (first entry) Murine ICE-ced-3 homologue. mIch-2; murine ICE-ced-3 homologue; programmed cell death; MED SH

RESULT

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Gaps

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RESULT

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New agoutis 37.08.

New agoutis 19,081.

Taltering melanin prodn., for treating e.g. melasma photo-ageing altering melanin prodn., for treating e.g. melasma photo-ageing spots, solar keratosis or vitilish.

The sequences given in W10101-29 are biologically active peptides and fragments of the agouti signaling protein (ASP) which have and fragments of the agouti signalling protein (ASP) which have depigmenting activity. These peptides are useful for cosmetic purposes and fragmentary conditions in the prevention or treatment of various hyperpigmentary conditions and diseases such as melasma photoageing spots, solar keratosis, and post-inflammatory hyperpigmentation such as occurs at sites of wound healing. They can also be used to provide enhanced eumelanogenesis for treating eg. vitilingo, leucoderma, some
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-5EP-1997 (first entry)
Human agouti signalling protein fragment #2.
Human agouti signalling protein; ASP; depigmenting activity; cosmetic;
Agouti signalling protein; ASP; depigmenting activity; cosmetic;
hyperpigmentary condition; melasma photoagaing spots; solar keratosis;
post-inflammatory hyperpigmentation; wound healing; eumelanogenesis;
vitiligo; leucoderma; albinism; hair greying.
Homo sapiens.
w09700892-A2.
                                                                                                                                     DNA corresp. to (part of) foot and mouth disease virus RNA - useful in prepn. of vaccines for producing antibodies against the virus Example; Fig 6; 57pp; English.

The inventors claim a DNA molecule comprising a nucleotide sequence corresp. to a portion of foot-and-mouth disease virus RNA (FMDV). The DNA molecule is esp. for a precursor of FMDV capsid protein. It esp. codes for FMDV protein p88 and VPI-VP4. It may code for why VP2, VP3 and VPI contiguously. The inventors also claim a vaccine for stiumlating prodn. of antibodies against FMDV in a mammal which comprises at least one of the above recombinant proteins produced by a host cell transformed with the DNA.
(NAIR ) National Res Dev Corp.

(WELL ) Wellcome Foundation Ltd.

Boothroyd JC, Cross GaM, Highfield PE, Winther MD, Rowlands DJ,

Brown F, Harris TJR, Lowe PA;

WPI; 82-26702E/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 64; DB 23; Length 45; Pred. No. 8.59e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 65; DB 5; Length 78; Pred. No. 7.06e+01; 9; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-JAN-1997.
21-JUN-1996; U10695.
23-JUN-1995; US-000436.
(USSH ) US DEPT HEALTH 6 HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 OKTCSCRLYELLHGAGNHAAGILT 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
ID W10105 standard; protein; 45 AA.
AC W10105;
DT 17-SEP-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45 qntcsthtyqglhst-thstlvls 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UT 8
W10106 standard; protein; 45
W10106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 25.4%;
Best Local Similarity 37.5%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Match 25.0%; Local Similarity 41.2%; Local 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 papaccdpcascqcrff 32
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                                                                                                                         N-PSDB; N20019
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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       or dental anomalles, induction
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                     of local endochondral bone formation in non-union fractures, peridontal applens. requiring bone formation and cartilage repair, eg in the treatment of osteoarthritis.

See also P95679-P95692 and N95097.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human mature unidate diphosphate galactose-4-epimerase (UDP-G4E) (W01619) catalyses a reversible reaction between UDP-glucose and UDP-galactose that allows galactose residues to enter into the main pathways of glucose metabolism. A deficiency of the enzyme results in galactosaemia. The amino acid sequence of UDP-G4E was deduced from a cDNA clone (T58301) derived from a human endometrial tumour library. Recombinant UDP-G4E polypeptides can be produced in transformed host (e.g. E. coli, COS, Sf9 insect) cells or expressed in vivo for use in the treatment of UDP-G4E deficiency, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding human uridine diphosphate galactose-4-epimerase - used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human uridine diphosphate galactose-4-epimerase.
Uridine diphosphate galactose-4-epimerase; UDP-G4E; galactosaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence of a foot and mouth disease virus capsid protein encoded by a region of recombinant plasmid pFA61/t76 Yocchne, antibody, capsid protein; immunogen; antigen; foot and mouth disease virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 66; DB 20; Length 340. Pred. No. 5.80e+01;
                                                                                                                                                                    Score 66; DB 1; Length 102;
Pred. No. 5.80e+01;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in the treatment and diagnosis of galactosaemia Claim 1; Page 43-44; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                     JT 6
W01619 standard; Protein; 348 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P20020 standard; Protein; 78 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25.8%;
53.8%;
                                                                                                                                                                  25.8%;
Similarity 56.3%;
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                   34 cpyplyeilngs-nha 48
                                                                                                                                                                                                                                                                                                          12 CSCRLYELLHGAGNHA 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GB-030208.
GB-034130.
GB-038147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-NOV-1996.
11-MAY-1995; U05785.
11-MAY-1995; WO-U05785.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GB-011064.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   W01619;
24-APR-1997 (first
                                                                                                                                                                       Query Match
Best Local Similarity
Matches 9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
lest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J1 H, Rosen CA;
WPI; 96-518666/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        348 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; T58301.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qalactosaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-APR-1981;
18-AUG-1981;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-SEP-1980;
22-OCT-1980;
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                                                                                                                           Sequence
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6; Indels

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Best Loca Matches

В à

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particularly plants for the control of nematodes claim 4; Page 35-39; 44pp; English.

This sequence represents the protein encoded by a polynucleotide of the invention. The polynucleotide of the invention is a sequence from a Bacillus thuringiensis (Bt) isolate selected from PS80JJ1, PS158D5, PS167P, PS167E, PS177F1, PS177G, PS204G4 and PS204G6, that encodes a toxin active against nematodes This sequence represents the 167P protein, and is a delta-endotoxin protein. The polynucleotides and toxins can be used for the control of nematode pests such as Panagrellus
                                                                                                                                                                                                                                                                                                                                                                                                                                     New agouti signal protein peptide(s) and nucleic acids - used for altering melanin prodn., for treating e.g. melasma photo-ageing pepts, solar keratosis or vitiligo
Claim 5; Page 8-9; 67pp; English.
The sequences given in W10101-29 are biologically active peptides and fragments of the agouti signalling protein (ASP) which have depigmenting activity. These peptides are useful for cosmetic purposes and for clinical application in the prevention or treatment of various hyperpigmentary conditions and diseases such as melasma photoageing spots, solar keratosis, and post-inflammatory hyperpigmentation such as occurs at sites of wound healing. They can also be used to provide enhanced eumelanogenesis for treating eg. vitiligo, leucoderma, some forms of albinism and hair greying.
    Agouti signalling protein; ASP; depigmenting activity; cosmetic; hyperplymentary condition; melasma photcageing spots; solar Keratosis; post-inflammatory hyperplymentation; wound healing; eumelanogenesis; vitiligo; leucoderma; albinism; hair greying.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-Apr-1998 (first entry).
Nematode toxin 1679-protein.
PCR primer; amplify; nematode toxic protein; Bacillus thuringiensis; delta-endotoxin gene; nematode pest control; Panagrellus redivivus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 8.59e+01;
3; Mismatches 6; Indels
                                                                                                                                                                                                                                                            /note= "Start of Cysteine-rich motif"
                                                                                                                                                                                                               "Start of basic region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 64; DB 23;
                                                                                                                                 1..21
/note= "Signal sequence"
32
                                                                                                                                                                                                                                                                                                                                                   23-JUN-1995; US-000436.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                     Location/Qualifiers
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W31504 standard; Protein; 1167
W31504;
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hes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102 papaccdpcascqcrff 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MYCO ) MYCOGEN CORP.
Fu J, Narva KE, Payne J;
WPI; 97-480163/44.
N-PSDB; T89185.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-SEP-1997.
21-MAR-1997; U04755.
21-MAR-1996; US-590554.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          167P protein.
Bacillus thuringiensis.
WO9734926-A2.
                                                                                                                                                                                                                 /note-
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23-JUN-1995; US-0004
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                                                                                                                                                                                                                                                                                                                                                                                                Hearing VJ;
WPI; 97-087323/08.
                                                                                              Mus musculus.
                                                                                                                                                                                                                                                                                   WO9700892-A2
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                           peptide
                                                                                                                                                                                            region
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Claim 6; Page 8-9; 67pp; English.

The sequences given in W10101-29 are biologically active peptides and fragments of the agouti signalling protein (ASP) which have depigmenting activity. These peptides are useful for cosmetic purposes and for clinical application in the prevention or treatment of various hyperpigmentary conditions and diseases such as melasma photoageing spots, solar keratosis, and post-inflammatory hyperpigmentation such as occurs at sites of wound healing. They can also be used to provide enhanced eumelanogenesis for treating eg. vitiligo, leucoderma, some
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-SEP-1997 (first entry)

Human agouti signalling protein.

Agouti signalling protein; ASP; depigmenting activity; cosmetic;

Agouti signalling protein; ASP; depigmenting activity; cosmetic;

hyperpigmentary condition; melasma photoageing spots; solar keratosis;

post-inflammatory hyperpigmentation; wound healing; eumelanogenesis;

vitiligo; leucoderma; albinism; hair greying.
Example; Page 17; 28pp; English.

The sequence is that of a polypeptide present in fraction K of the venom of Agelenopsis aperta, it blocks calcium channels in cells of both mammals and invertebrates, partic. those affecting neuronal and muscle cells. It may be used in the treatment of angina, hypertension, cardiomyopathies, supraventricular arrhythmia, coesophogeal achalasia, premature labour, and Raynaud's disease. It may also be of use in the study of cell physiology and in the control of invertebrate pests. It may be produced synthetically.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 64; DB 23; Length 130
Pred. No. 8.59e+01;
3; Mismatches 6; Indels
                                                                                                                                                                                                                                                         Score 64; DB 8; Length 48; Pred. No. 8.59e+01; 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Start of Cysteine-rich motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Start of basic region"
86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "Signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-JUN-1995; US-000436.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         forms of albinism and hair greying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ULT 13
W10102 standard; protein; 130 AA.
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Murine agouti signalling protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        n 14
W10101 standard; protein; 131 AA.
                                                                                                                                                                                                                                                         25.0%;
larity 45.5%;
Conservative
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Matches 7; Conservative
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23-JUN-1995; US-0004
                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                   19 ccrgrpcrcsm 29
                                                                                                                                                                                                                                                                                                                                                                                             6 CCRQKTCSCRL 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hearing VJ;
WPI; 97-087323/08.
                                                                                                                                                                                                                 48 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9700892-A2
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region region

RESULT ID W1 AC W1 DT 17

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Gaps

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Length 131;

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu Jul 30 09:30:53 1998; MasPar time 3.09 Seconds 267.875 Million cell updates/sec sular output not generated. ou:

>US-08-938-548A-11 (1-33) from USO8938548A.pep 256 1 QPLPDCCRQKTCSCRLYELLHGAGNHAAGILIL 33 Title: Description: Perfect Score:

Sequence:

PAM 150 Gap 11 Scoring table:

69111 seqs, 25083644 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

Statistics:

swiss-prot35 1:swiss1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 31.693; Variance 44.992; scale 0.704

SUMMARIES

Pred. No.	5.12e-02	1.20e-01	2.76e-01	4.17e-01	6.26e-01	6.26e-01	1.40e+00	1.40e+00	2.07e+00	2.07e+00	2.07e+00	2.07e+00	3.06e+00	3.06e+00	4.51e+00	4.51e+00	4.51e+00	4.51e+00	4.51e+00	4.51e+00	4.51e+00	6.60e+00	6.60e+00
Description	CASPASE-11 PRECURSOR (PUTATIVE TRANSMEMBRANE	PUTATIVE ACID PHOSPHAT	60S RIBOSOMAL PROTEIN	SPERM MITOCHONDRIAL CA	PUTATIVE FORKHEAD-RELA	IG ALPHA CHAIN C REGIO	MEIOTIC RECOMBINATION	UDP-GLUCOSE 4-EPIMERAS	UDP-GLUCOSE 4-EPIMERAS	PHOSPHORIBOSYLAMINOIMI	INTERFERON-ACTIVATABLE	HYPOTHETICAL PROTEIN M	MITOCHONDRIAL INHERITA	OMEGA-AGATOXIN IIIA.	OMEGA-AGATOXIN IVB PRE	BOLA PROTEIN HOMOLOG.	AGOUTI SWITCH PROTEIN	AGOUTI SWITCH PROTEIN	AGOUTI SWITCH PROTEIN	VACUOLAR PROCESSING EN	PROTEIN ECSC.	ANGIOTENSINOGEN PRECUR
E C	ICEB_MOUSE	NMA_HUMAN	PPAW_CAEEL	R10A_TRYBR	MCS_MOUSE	YUL2_CAEEL	ALC_RABIT	RE11_SCHPO	GALE_RAT	GALE_HUMAN	PURK_PSEAE	IFI5_MOUSE	Y115_METJA	MD12_SCHPO	TX03_AGEAP	TX4B_AGEAP	BOLA_HAEIN	AGSW_VULVU	AGSW_MOUSE	AGSW_HUMAN	VPE_VICSA	ECSC_BACSU	ANGT_MOUSE
DB	-	Н	-	Н	н	Н	Н	Н	-	Н	Н	Н	Н	-	Н	Н	Н	-	Н	-1	Н	Н	Н
Length	373	260	450	214	197	461	299	923	347	348	360	425	155	273	9 2	83	103	125	131	132	493	236	477
& Query Match	29.3	28.5	27.7	27.3	27.0	27.0	26.2	26.2	25.8	25.8	25.8	25.8	25.4	25.4	25.0	25.0	25.0	25.0	25.0	25.0	25.0	24.6	24.6
Score	75	73	71	70	69	69	49		99	99	99	99	65	65	64	64	64	64	64	64	64	63	63
Bosult No.	Н	~	e	4	'n	φ	7	ω	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23

DB 1; Length 373;

29.3%; Score 75;

Query Match

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	0.4909.9	9.61e+00	9.61e+00	9.61e+00	9.61e+00	9.61e+00	1.39e+01	1.39e+01	1.39e+01	1.39e+01	1.39e+01	1.39e+01	1.39e+01	1.39e+01	2.01e+01	2.01e+01	2.01e+01	2.01e+01	2.01e+01	2.01e+01	2.01e+01	2.01e+01
	TETRACYCLINE RESISTANC	UNC-6 PROTEIN PRECURSO	GLUTAMATE (NMDA) RECEP	GLUTAMATE (NMDA) RECEP	SPA2 PROTEIN.	MYOSIN HEAVY CHAIN, NO	GENE 34 PROTEIN.	UREASE OPERON URED PRO	UREASE OPERON URED PRO	HYPOTHETICAL PROTEIN K	TUBULIN BETA CHAIN.	PRPD PROTEIN.	GLYCINE BETAINE TRANSP	DNA REPAIR PROTEIN RAD	HYPOTHETICAL 37.9 KD P	MITOGEN-ACTIVATED PROT	HYPOTHETICAL 51.7 KD P	TETRACYCLINE RESISTANC	HYPOTHETICAL 118.6 KD	DNA POLYMERASE (EC 2.7	HYPOTHETICAL 133.0 KD	THYROGLOBULIN PRECURSO
	TET9_ENTFA	UNC6_CAEEL	NME1_RAT	NME1_MOUSE	SPA2_YEAST	MY SO_HUMAN	VG34_HSVEB	URED_KLEAE	URED_KLEPN	Y129_HUMAN	TBB_TRYBR	PRPD_SALTY	BETP_CORGL	RAD5_YEAST	YHO5_YEAST	NTF6_TOBAC	YMT1_CAEEL	TETM_UREUR	YAF3_SCHPO	DPOL_ADE07	YIC6_YEAST	THYG_BOVIN
	1		~	-1	Н	Н	Н	Н	Н	Н	н	Н	-	Н	н		н	Н	.	Н	Н	Н
	639	612	1464	1464	1466	1976	160	270	270	406	442	483	595	1169	334	371	471	639	1039	1122	1150	2769
,	24.6	24.2	24.2	24.2	24.2	24.2	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.4	23.4	23.4	23.4	23.4	23.4	23.4	23.4
	63	62	62	62	62	62	61	61	61	61	61	61	61	61	9	9	9	9	9	9	9	9
	24	25	. 36	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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-!- THIS IMMUNOCLOBULIN BELONGS TO THE IGA-G SUBCLASS. IT WAS ISOLATED FROM A RABBIT HOMOZYGOUS FOR A2, N80, DE12,15, F71, G75 HEAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
KNIGHT K.L., MARTENS C.L., STOKLOSA C.M., SCHNEIDERMAN R.D.;
NUCLEIC ACIDS RES. 12:1657-1670(1984).
-!- FUNCTION: IG ALPHA IS THE MAJOR IMMUNOGLOBULIN CLASS IN BODY
SECRETIONS. IT MAY SERVE BOTH TO DEFEND AGAINST LOCAL INFECTION
AND TO PREVENT ACCESS OF FOREIGN ANTIGENS TO THE GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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NUCLEIC ACIDS RES. 18:5289-5289(1990).
-1- FUNCTION: CATALYZES TWO DISTINCT BUT ANALOGOUS REACTIONS: THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RATTUS NORVEGICUS (RAI).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1990 (REL. 16, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP-GALACTOSE 4-EPIMERASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 67; DB 1; Length 923;
Pred. No. 1.40e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 67; DB 1; Lo
Pred. No. 1.40e+00;
4; Mismatches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 923 AA; 107418 MW; B51C7725 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                  594CED7C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
MEIOTIC RECOMBINATION PROTEIN REC11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE; 97231330.
LI Y.F., NUMATA M., WAHLS W.P., SMITH G.R.;
MOL. MICROBIOL. 23:869-878(1997).
MEIOSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              923 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                232 CCDIMRCLCLIVNKLSEKSNQTAEILVL 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 CCRQKTCSCRLYELLHGAGNHAAGILTL 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                  299 AA; 32256 MW;
                                                                                                                                                                                                                                                                                                        HSSP; P01857; 1PFC.
PROSITE; PS00290; IG_MHC; 2.
IMMUNOGLOBULIN C REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 35.7%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.2%;
Similarity 50.0%;
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                            CHAIN HAPLOTYPE.
EMBL; X00353; G1576; -.
PIR; A02174; AHRB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE-SKELETAL MUSCLE;
MEDLINE; 90384840.
                                                                                                                                           IMMUNOLOGIC SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 PLPDCCRQKTC-SC 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44 PFPDCCPANSCCTC 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RE11_SCHPO
Q92380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CT 9
GALE_RAT
P18645;
                                                                                                                                                                                                                                                                                                                                                                                              NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT TO SERVICE TO S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
             S T W D D C C C C C C C L B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
1G ALPHA CHAIN CREGION (FRAGMENT).
0RYCTOLAGUS CUNICULUS (RABBIT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
  STRUCTURE OF THE SPERM MITOCHONDRIA.

-1 - SUBCELLUIAR LOCATION: KERATINOUS MITOCHONDRIAL CAPSULE.

-1 - TISSUE SPECIFICITY: TESTIS.

-1 - DEVELOPMENTAL STAGE: LATE MEIOFIC AND EARLY HAPLOID CELLS.

EMBL; M88463; G457886; -:

EMBL; M30603; G567228; -.

PIR; A37199; A37199.

HSSP; P01058; ITAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 69; DB 1; Length 461;
Pred. No. 6.26e-01;
6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                     MITOCHONDRION; SELENIUM; SPERM; TESTIS; SPERMATOGENESIS.
BINDING 7 7 SELENIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
101-NOV-1997 (REL. 35, LAST ANNORATION UPDATE)
PUTATIVE FORKHEAD-RELATED TRANSCRIPTION FACTOR F26A1.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBMITTED (JUN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; UZ7312; G860601.
WORMER; T26A1.2; G802683.
PROSITE; PS01657; FORK_HEAD_1; 1.
PROSITE; PS01658; FORK_HEAD_2; 1.
PROSITE; PS01058; FORK_HEAD_2; 1.
HYPOTHERICAL PROTEIN; DNA-BINDING; NUCLEAR PROTEIN; TRANSCRIPTION REGULATION.
PINA, BIND 171 262 FORK-HEAD.
SEQUENCE 461 AA; 54171 MW; FB2C3787 CRC32:
                                                                                                                                                                                                                                                                                                                                                                                                               Score 69; DB 1; Le
Pred. No. 6.26e-01;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                 SELENIUM.
SELENIUM.
SELENIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
-1- SIMILARITY: CONTAINS A FORK-HEAD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           461 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         299 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                              34 34 Si
197 AA; 21015 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 27.0%;
Best Local Similarity 35.3%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 71.4%;
10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     27.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            221 RHVLCKCQLFDVLQVEG 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 ROKTCSCRLYELLHGAG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 PLKPPCCPQK-CSC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 PL-PDCCRQKTCSC 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EUTHERIA; LAGOMORPHA.
                                                                                                                                                                                                                       MGD; MGI:96945; MCS
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 10; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-BRISTOL N2; FULTON L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
MEDLINE; 84144059.
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LT 6 YUL2_CAEEL Q19802;

RESULT

SEQUENCE BINDING

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ALC_RABIT P01879;

RESULT

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SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GCCANE J.D.,
KERLANGE A.R., DOUGHERTY B.A., TOMB J.-F., ADAMS M.D., REICH C.I.,
OVERBEEK R., KIRKNESS E.F., WEINSTOCK K.G., MERRICK J.M., GLODEK A.,
SCOTT J.L., GEOGHAGEN N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D.,
UTTERBACK T.K., KELLEY J.M., PETERSON J.D., SADOW P.W., HANNA M.C.,
COTTON M.D., ROBERTS K.M., HURST M.A., KAINE B.P., BORODOVSKY M.,
KLENK H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                METHANOCOCCUS JANNASCHII.
ARCHAEBACTERIA; EURYARCHAEOIA; METHANOCOCCALES; METHANOCOCCACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 65; DB 1; Length 155;
Pred. No. 3.06e+00;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 65; DB 1; Length 273;
Pred. No. 3.06e+00;
6; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BERGER K.H., SOGO L.F., YAFFE M.P.;
SUBMITTED (NOV-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-IS MILLARITY: TO YEAST MDM12.
EMBL; UG4674; G1655884; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                155 AA; 17727 MW; 9D9D61E8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          273 AA; 30517 MW; 9024B3CC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-1993 (REL. 27, CREATED)
01-0CT-1993 (REL. 27, LAST SEQUENCE UPDATE)
01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
0MEGA-AGATOXIN IIIA.
                                                                                                              01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
HYPOTHETICAL PROTEIN MJ0115.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              273 AA.
                                         155 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MITOCHONDRIAL INHERITANCE COMPONENT MDM12. MDM12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25.4%;
ilarity 53.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25.4%;
Similarity 53.3%;
8; Conservative
                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 CCKITKPCPYRDYEL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 CCR-QKTCSCRLYEL 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U67469; G1498882;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               213 LLHGTGEHASSVI 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 LLHGAGNHAAGIL 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 96337999
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Q92377;
                                  Y115_METJA
057579;
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P33034;
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RESULT TO THE PROPERTY OF THE 
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FUNCTION: OMEGA-AGATOXIN ARE ANTAGONIST OF VOLTAGE-SENSITIVE
-!- FUNCTION: OMEGA-AGATOXIN ARE ANTAGONIST OF VOLTAGE-SENSITIVE
CALCIUM CHANNELS. THEY BLOCK INSECT NEUROMUSCULAR TRANSMISSION
PRESYNAPPITGALLY. POTENT BLOCKER OF N- AND L-TYPE CALCIUM CHANNELS.
-!- PIM: SIX DISULFIDE BONDS ARE PRESENT (PROBABLE).
PIR; A42335; A42335.
VENOM; NEUROTOXIN; CALCIUM CHANNEL INHIBITOR; PRESYNAPTIC NEUROTOXIN.
SEQUENCE 76 AA; 8518 MW; C7EAOE12 CRC32;
                                                                                                                      VENEMA V.J., SWIDEREK K.M., LEE T.D., HATHAWAY G.M., ADAMS M.E.;
J. BIOL. CHEM. 267:2610-2615(1992).
AGELENOPSIS APERTA (FUNNEL-WEB SPIDER).
EUKARYOTA; METAZOA; ARTHROPODA; CHELICERATA; ARACHNIDA; ARANEAE
                                                                                                                                                                                                                                                                                                                                Length 76;
                                                                                                                                                                                                                                                                                                                              Score 64; DB 1; L
Pred. No. 4.51e+00;
                                                                                                                                                                                                                                                                                                                                                                        6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: Thu Jul 30 09:31:09 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                              5 DCCROKT-CSC-RLYELLHGA 23
                                                                                                                                                                                                                                                                                                                                                                                                                17 QCCRRNGYCSCYSLFGYLKSG 37
                                                                                                                                                                                                                                                                                                                              Query Match 25.0%;
Best Local Similarity 38.1%;
Matches 8; Conservative
                                                                                                     92129351
                                                                                  TISSUE-VENOM;
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu Jul 30 09:31:28 1998; MasPar time 5.40 Seconds 257.359 Million cell updates/sec :uo d

>US-08-938-548A-11 (1-33) from USO8938548A.pep 256 1 QPLPDCCRQKTCSCRLYELLHGAGNHAAGILTL 33 ular output not generated. Title: Description: Perfect Score:

Sequence:

PAM 150 Gap 11 Scoring table:

140542 segs, 42109429 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

sptrembl5
1:sp_fung1 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_mbc at 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Mean 30.295; Variance 46.908; scale 0.646 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Score Match Length DB ID 77 30.1 363 4 002839 74 28.9 753 4 002839 73 28.5 1876 3 022187 73 28.5 1876 3 024453 73 28.5 1876 3 024453 72 28.1 147 10 061639 70 27.3 426 9 03357 70 27.3 426 641 9 048712 68 26.6 646 9 048712 66 25.8 479 9 P94426 65 25.4 137 4 028584 65 25.4 137 4 028584 65 25.4 310 3 001473 64 25.0 359 9 P75863 64 25.0 398 3 018373			dР					
77 30.1 363 4 002833 74 28.9 750 3 093473 73 28.5 1876 3 024453 73 28.5 1876 3 024453 72 28.1 1876 3 024453 72 28.1 187 0 061639 72 28.1 187 9 03367 70 27.3 426 3 001969 70 27.3 426 3 001969 70 27.3 483 1 091893 68 26.6 641 9 048712 66 25.8 4197 9 994426 65 25.4 197 4 028584 64 25.0 369 9 775863 64 25.0 369 9 775863 64 25.0 369 3 701873	Result No.	Score	Query Match	Length	DB	OI OI	Description	Pred. No.
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0 398 3 018373	19	64	25.0		6	044258	1-CARBOXY-3-CHLORO-3,4	8.38e+00
	20	64	25.0	398	m	018373	SELD PROTEIN.	8.38e+00

8.38e+00 1.21e+01	1.21e+01	1.21e+01	1.21e+01	1.21e+01	1.21e+01	1.21e+01	1.21e+01	1.21e+01	1.21e+01	1.21e+01	1.21e+01	1.73e+01	1.73e+01	1.73e+01	1.73e+01	1.73e+01	1.73e+01	1.73e+01	1.73e+01	1.73e+01	1.73e+01	2.47e+01	2.47e+01
SELENOPHOSPHATE SYNTHE REPRESSOR/INDUCER PROT	COSMID C27A2.	RIBONUCLEASE.	T21B10.6.	F21C3.1.	AMINO ACID TRANSPORTER	TETRACYCLINE RESISTANC	TETRACYLINE RESISTANCE	ORF11.	TETM GENE.	LET 858.	SIMILARITY TO EGF-LIKE	NONMUSCLE MYOSIN HEAVY	NONMUSCLE MYOSIN HEAVY	NONMUSCLE MYOSIN HEAVY	DNA FOR DNAJ, COMPLETE	NONMUSCLE MYOSIN HEAVY	NONMUSCLE MYOSIN HEAVY	T24D5.1.	N-METHYL-D-ASPARTATE R	N-METHYL-D-ASPARTATE R	N-METHYL-D-ASPARTATE R	TRKB (FRAGMENT).	MYOSIN HEAVY CHAIN, NO
018597	018238	004393	922627	019671	039135	053770	067709	057224	047810	017336	018857	027991	012989	027990	033700	062707	062706	022732	012879	063728	008948	091373	002015
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21 22	23	24	25	26	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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WATERSTON R.;
                                                        RESULT 9
1D 001969
1D 001969
1D 01-JUL-1
DT 01-JUL-1
DT 01-JUL-1
DE SIMILAR
GN MOIDT-4-
CS CAENORHA
CC EUKARYOT
RN [1]
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Q91493;
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SUBMITTED (OCT-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-1- CATALYTIC ACTIVITY: ATP-DEPENDENT BREAKAGE, PASSAGE AND REJOINING
OF DOUBLE-STRANDED DAY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POIRIER F., CHAN C.T.J., TIMMONS P., ROBERTSON E.J., EVANS M.J. RIGBY P.W.J.; DEVELOPMENT 113:1105-1114(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
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                                                                                                                                             Score 73; DB 3; Length 1876;
Pred. No. 2.65e-01;
5; Mismatches 8; Indels
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Pred. No. 3.94e-01;
2; Mismatches. 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 3.94e-01;
9; Mismatches 10; Indels
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PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; MYXOBACTERALES;
MYXOCOCCACEAE.
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LAST ANNOTATION UPDATE)
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LAST ANNOTATION UPDATE)
                                                                                           DF107ECF CRC32;
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PROSITE; PS00177; TOPOISOMERASE_II; 1.
ISOMERASE; TOPOISOMERASE; AIP-BINDING.
SEQUENCE 815 AA; 89636 MW; 65A25520 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X58196; G51133; -. SEQUENCE 147 AA; 16309 MW; 6DC857F5 CRC32;
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J. BIOL. CHEM. 271:13892-13899(1996)
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                                                                                                                                                                                                                                                                                                                 EMBL; U52192; G1272420; --
FLYBASE; FBGN0015278; P13K6BD.
SEQUENCE 1876 AA; 210505 MW;
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01-NOV-1996 (TREMBLREL. 01,
01-NOV-1996 (TREMBLREL. 01,
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ilarity 32.1%;
Conservative
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-JAN-1998 (TREMBLREL. 05,
-JAN-1998 (TREMBLREL. 05,
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Similarity 59.1%;
13; Conservative
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Best Local Similarity 41.7%;
Matches 10; Conservative
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01-JAN-1998 (TREMBLREL.
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MEDLINE; 92249159.
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033367;
033367;
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Q61639
Q61639;
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BONFIELD J., BURTON J., CONNELL M., COPERT T., COOPER J., COLLSON A., CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L., CARRINO M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L., GARDNER A., GREEN P., LANGIER L., JOHNSTON L., JOHNS M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M., PARGNON J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R., SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SURJERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R., WATENSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
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BUKRYOTA: METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
CHONDRICHTHYES.
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Pred. No. 8.65e-01;
....matches 7; Indels
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GATTUNG S., GOELA D., WILSON R.;
SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
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EMBL; AF003739; G2105488; --
PROSITE; PS00627; GHMA_KINA-ES_ATP; 1.
SEQUENCE 426 A3, 47290 MW; 7CBEF743 CRC32;
                                             CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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01, LAST SEQUENCE UPDATE)
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XEADON J.E., LIN H., DYER S.M., BURDEN S.J.;
J. CELL BIOL. 115:1069-1076(1991).
426 AA
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J. PHYSIOL. (PARIS) 0:131-133(1991).
EMBL, M37645; G397971; -.
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NON_TER 1.
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(TREMBLREL. 04, I
(TREMBLREL. 05, I
PRELIMINARY;
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Best Local Similarity 48.1%;
Matches 13; Conservative
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01-JUL-1997 (TREMBLREL. 0
01-JAN-1998 (TREMBLREL. 0
SIMILAR TO GALACTOKINASE.
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01-NOV-1996 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
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MEDLINE; 94150718.
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01-NOY-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOY-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
KAPS.5 KERATIN PROTEIN (FRAGMENT).
KRTAPS.5. STRES (SHEEP).
OVIS ARTES (SHEEP).
EUTHERIA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                            Score 66; DB 9; Length 479;
Pred. No. 3.99e+00;
5; Mismatches 5; Indels
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STRAIN-168;
KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; 299106; E1182356; -.
SEQUENCE 479 AA; 55166 MW; 3C2D1F5A CRC32;
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TISSUE-WOOL FOLLICLE;
MEDLINE; 94358466.
JENKINS B.J., POWELL B.C.;
J. INVEST. DERMATOL. 103:310-317(1994).
EMBL; X73435; G313722; -..
                                                                                                                                            Query Match 25.8%;
Best Local Similarity 41.2%;
Matches 7; Conservative
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15 RLYELLHGAGNHAAGIL 31
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Q28584
Q28584;
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arch completed: Thu Jul 30 09:31:53 1998 time: 25 secs.

87 VPVCCRVPACSC 98 :| || :||| 3 LPDCCRQKTCSC 14

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MasPar time 4.56 Seconds 216.418 Million cell updates/sec MPsrch_pp

Thu Jul 30 09:23:30 1998; bular output not generated. >US-08-938-548A-9 (1-27) from USO8938548A.pep 192 1 PGPPGLQGRLQRLLQANGNHAAGILIM 27 Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

Searched:

120441 seqs, 36531193 residues

Minimum Match 0% Listing first 45 summaries Post-processing:

pir56

Database:

Mean 29.905; Variance 54.628; scale 0.547 Statistics:

1:pirl 2:pir2 3:pir3 4:pir4 5:nrl3d

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Pred. No.	5.23e+00	5.23e+00	7.27e+00	7.27e+00	7.27e+00	7.27e+00	7.27e+00	7.27e+00	7.27e+00	7.27e+00	7.27e+00	1.01e+01	1.01e+01	1.01e+01	1.39e + 01	1.39e+01	1.91e+01	1.91e+01	1.91e+01	1.91e+01	1.91e+01	1.91e + 01	2.62e+01
	•	Description	mALDP protein - mouse	hypothetical protein	hypothetical protein	superoxide dismutase	superoxide dismutase	transcription initiat	PAS1 protein - yeast	'n	hypothetical protein	RNA-directed DNA poly	adenylate cyclase (EC	fatty-acid synthase (hypothetical protein	hypothetical protein	protein-tyrosine-phos	protein-tyrosine-phos	sulfite reductase (fe	YOR1 protein - yeast	hrpE protein - Pseudo				
		A :	S47044	H64888	E69913	A41654	B41654	JH0496	S11712	S41307	JN0443	JN0445	A55152	D69081	549183	S19248	A33988	G01880	S25618	S51155	A46101	B46101	RDYCS7	S64616	S61858
		B :	7	~	~	7	7	7	~	~	7	~	~	7	~	٦	~	N	7	~	~	7	Н	7	7
	•	Match Length DB	736	879	178	187	187	442	442	510	525	528	1157	150	253	319	1692	2509	239	263	535	548	624	1477	439
æ	Query	Match	35.4	35.4	34.9	34.9	34.9	34.9	34.9	34.9	34.9	34.9	34.9	34.4	34.4	34.4	33.9	33.9	33.3	33.3	33.3	33.3	33.3	33.3	32.8
		Score	89	89	67	67	67	67	67	67	67	67	67	99	99	99	65	65	64	64	64	64	64	64	63
	Pesult	No.		7	m	4	'n	9	7	œ	0	10	11	12	13	14	15	16	17	18	19	20	21	22	23

hypothetical protein 2.62e+01 hypothetical protein 2.62e+01 eddysone receptor - 6.62e+01 allergen TBA-1 - Toxo 3.59e+01 hypothetical protein 3.59e+01 hypothetical protein 3.59e+01 factor VIII-associate 3.59e+01 hypothetical protein 3.59e+01 transcription initiat 3.59e+01 transcription initiat 3.59e+01 transcription initiat 3.59e+01 collagen alpha 4(IV) 3.59e+01 collagen alpha 2(IV) 3.59e+01 hypothetical protein 4.89e+01 beta-globulin B precu 4.89e+01 B-alpha pheromone-rec 4.89e+01	#common_name house mouse ision 13-Jan-1995 #text_change Sadoulet, H.; Garnier, J.M.; Mandel, a Library, May 1994 e homologue of the X-linked ne. g520954; PID:g520955 eight 81858 #checksum 1613	.68; DB 2; Length 736; No. 5.23e+00; Mismatches 10; Indels 0; Gaps 0;
32.8 702 2 C64935 32.8 7702 2 C64935 32.8 7702 2 C64935 32.8 378 2 A41055 32.3 256 1 Q3YCRQ 32.3 256 1 Q3YCRQ 32.3 380 2 A42835 32.3 400 2 S76529 32.3 460 2 S76229 32.3 460 2 S76229 32.3 1690 2 C6411B 32.3 1690 2 C6411B 32.3 1690 2 C64916 31.8 248 1 LNHUP6 31.8 248 1 LNHUP6 31.8 255 S12255 31.8 258 1 EWCKBB 31.8 258 1 EWCKBB 31.8 258 1 S69562 31.8 259 2 S12255 31.8 259 2 S12255 31.8 259 2 S12255 31.8 516 1 FWCKBB	#type complete nal_name Mus musculus nal_name Mus musculus sap-1997 sep-1997 44 44 45 c.O.; Thomas, J.; S. Litted to the EMBL Data sequence of the mouse renoleukodystrophy gen the probleminary nRNA nRNA nRNA nRNA ces EMBL:Z33637; NID:g	35.4%; Score larity 44.4%; Pred. Conservative 5;
	RESULT 1 ENTRY MALDI ORGANISM #form DATE 13-3 ACCESSIONS 8470 REFERENCE 8470 REFERENCE 8470 REFERENCE 8470 #authors 30 July #submission subm. #accession 8470 #status add. ##status ##status ##status ##molecule_type ##residues ##residues ##residues ##residues ##residues ##residues ##residues ##residues ##residues	Query Match Best Local Simi Matches 12;

A64720
Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.;
Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.;
Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.;
Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao, H64888 #type complete
hypothetical protein b1381 - Escherichia coli (strain K-12)
#formal_name Escherichia coli
12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change
14-Nov-1997 ACCESSIONS REFERENCE #authors N TITLE ORGANISM DATE RESULT ENTRY

704 AGIPKMOGRLOELROILGEAAAPVOPL 730 : | | : | | | | | : : 1 | BGPPGLQGRLQRLLQANGNHAAGILTM 27

셤 ò #journal Science (1997) 277:1453-1462
#title The complete genome sequence of Escherichia coli K-12.
#cross.references MUID:97426617
#accession H648Ba
#steatus preliminary; nucleic acid sequence not shown:

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                                                                                                                                                                                                                                                                                                               ##molecule_type DNA
#residues
##cross-references EMBL:X52983
##note the authors translated the codon CAG for residue 430 as
##note His and GGG for residue 431 as Pro
His and GGG for residue 431 as Pro
AT This protein is the functional homolog of the principal sigma
factors involved in the transcription of housekeeping genes.

    Streptomyces

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                                                                                                                                                                 Shiina, T.; Tanaka, K.; Takahashi, H. Gene (1991) 107:145-148
Sequence of hrdB, an essential gene encoding sigma-like
transcription factor of Streptomyces coelicolor A3(2):
homology to principal sigma factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #superfamily transcription initiation factor sigma katf;
transcription initiation factor sigma katf homology
DNA binding; sigma factor; transcription initiation
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                                              sigma-like transcription factor
#formal_name Streptomyces coelicolor
31.Mar-1992 #sequence_revision 31.Mar-1992 #text_change
24.Jul-1997
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03-May-1994 #sequence_revision 20-Feb-1995 #text_change
08-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #domain transcription initiation factor sigma katF
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442 #molecular-weight 48364 #checksum 4785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, May 1990
Multiple homolog genes for principal sigma subunit
Streptomyces coelicolor A3(2).
 JH0496 #type complete
transcription initiation factor sigma homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 442;
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##experimental_source strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tanaka, K.; Shiina, T.; Takahashi, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. No. 7.27e+00;
Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
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Pred. No.
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11; M
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#contents A3[2]
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Best Local Similarity 31.8%;
Matches 7; Conservative
                                      coelicolor
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##residues 1-44
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                                                    ALTERNATE_NAMES ORGANISM
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#title
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                                                                                                                                ACCESSIONS
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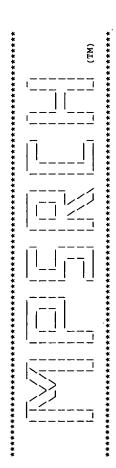
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S41307 #type complete transcription initiation factor sigma - Streptomyces griseus #formal_name Streptomyces griseus 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Sep-1997
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Gene (1992) 122:63-70.
Four genes in Streptomyces aureofaciens containing a domain
characterstic of principal sigma factors.
                                                                                                                                                                                                                                                                                                                                                                                                               Marcos, A.T.; Diez, B.; Gutierrez, S.; Fernandez, F.J.; Velasco, J.; Martin, J.F. submitted to the EMBL Data Library, December 1993 organization and expression of the hrdb-sprC gene cluster o streptomyces griseus encoding a signa factor protein and serine protease. Role on growth and sporulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              *superfamily transcription initiation factor sigma katF;
transcription initiation factor sigma katF homology
DNA binding; sigma factor; transcription initiation
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transcription initiation factor sigma katF homology
DNA binding; sigma factor; transcription initiation
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homology #label KTF
#length 525 #molecular-weight 57204 #checksum 9676
                             Gaps
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#length 510 #molecular-weight 55795 #checksum 1415
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##cross-references EMBL:X75952; NID:9440164; PID:9581664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 67; DB 2; Length 510;
Pred. No. 7.27e+00;
11; Mismatches 4; Indels
                          Indels
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##cross-references GB:M90411; NID:g153305; PID:g153306
. No. 7.27e+00;
Mismatches 4;
  Pred. 1
11; Mi
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                                                                          370 LQEQLHSVLDTLSEREAGVVSM 391
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LQGRLQRLLQANGNHAAGILTM 27
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                                                                                                             6 LOGRLORLLOANGNHAAGILTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              streptomyces.
  Best Local Similarity 31.8%;
Matches 7; Conservative
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Best Local Similarity 31.8%;
Matches 7; Conservative
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CLASSIFICATION
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1328-1413
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                                                                                                                                                                                                                                                                                                                                                                                                                                       #authors Herzer, P.J.; Inouye, S.; Inouye, M.
#journal Mol. Microbiol. (1992) 6:345-354
#title Retron Ecl07 is inserted into the Escherichia coli genome by
replacing a palindromic 34bp intergenic sequence.
#cross-references MUID:92204001
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Adenylate cyclases in yeast: a comparison of the genes from Schizosaccharomyces pombe and Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                 $19248  #type complete
RNA-directed DNA polymerase (EC 2.7.7.49), msDNA specific
Escherichia coli retron Ecl07
DNA nucleotidyltransferase (RNA-directed); reverse
transcriptase; revertese
#formal_name Escherichia coli retron Ecl07
20.Feb-1995, #sequence_revision 15-Oct-1996 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #journal Proc. Natl. Acad. Sci. U.S.A. (1989) 86:7989-7993
#fitle The adenylyl cyclase gene from Schizosaccharomyces pombe.
#accession A33988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         adenylate cyclase (EC 4.6.1.1) - fission yeast (Schizosaccharomyces pombe)
#formal_name Schizosaccharomyces pombe
23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change
09-sep-1997
                                                                                                Gaps
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#superfamily reverse transcriptase
nucleotidyltransferase
#length 319 #molecular-weight 36363 #checksum 2019
##cross-references EMBL:X79980; NID:9510451; PID:9510452
Y #Length 253 #molecular-weight 27305 #checksum 1526
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                                                   Score 66; DB 2; Length 253;
Pred. No. 1.01e+01;
5; Mismatches 10; Indels
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Pred. No. 1.01e+01;
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                                                                                                                                                          preliminary
                                                       34.4%;
ilarity 37.5%;
Conservative
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Best Local Similarity 50.0%;
Matches 9; Conservative
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S19248
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#title
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#cross-references MUID:89345533
#accession A33393
#status
#status
preliminary
##status
#recoss-references GB:M24942; NID:9173378; PID:9173379
##recoss-references GB:M24940; M319842; PID:9173378; PID:9173378; PID:9173378; PID:9173378; PID:9173378; PID:9173378; PID:9173379
##recoss-references GB:M247478; PID:9173378; PID:917337
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 09:24:01 1998; MasPar time 4.11 Seconds 164.767 Million cell updates/sec : uo u

bular output not generated.

>US-08-938-548A-9 (1-27) from US08938548A.pep 192 1 PGPPGLQGRLQRLLQANGNHAAGILIM 27 Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

69111 seqs, 25083644 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

swiss-prot35 1:swiss1

Statistics:

Mean 31.311; Variance 47.835; scale 0.655

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	1.44e+00	1.44e+00	2.09e+00	2.09e+00	2.09e+00	4.39e+00	4.39e+00	4.39e+00	6.32e+00	6.32e+00	6.32e+00	9.05e+00	9.05e+00	1.29e+01	1.29e+01	1.29e+01	1.29e+01	1.29e+01	1.29e+01	1.29e+01	1.83e + 01	1.83e+01
Description	<u> </u>	HYPOTHETICAL 96.8 KD P 1	SUPEROXIDE DISMUTASE L	RNA POLYMERASE PRINCIP	SI	CUTICLE COLLAGEN 36. 4	ADENYLATE CYCLASE (EC 4	THYROID RECEPTOR INTER 4	NTERLEUKIN-11 PRECURS (SULFITE REDUCTASE (FER 6	OLIGOMYCIN RESISTANCE (HYPOTHETICAL 78.9 KD P 9	SCDYSONE RECEPTOR (ECD 5	HYPOTHETICAL 28.7 KD P 1	FACTOR VIII INTRON 22 1	ARGININOSUCCINATE SYNT 1	RNA POLYMERASE SIGMA F 1	COLLAGEN ALPHA 4(IV) C 1	COLLAGEN ALPHA 2(IV) C 1	PROCOLLAGEN ALPHA 2(IV 1	HYPOTHETICAL PROTEIN M 1	NEGATIVE FACTOR (F-PRO 1
ID	}	YDBH_ECOLI HI		_		_	•	TR12_HUMAN TH		SIR_SYNP7 St	YOR1_YEAST OI	YCBY_ECOLI H	_	~	F812_MOUSE F1	ASSY_SYNY3 A	RPSD_CAUCR RI	CA44_HUMAN CC	CA24_CAEEL CO	CA24_ASCSU PI	Ā	NEF_HV2NZ NI
80	H		4 ~4	Н	m	н	H	-	-	Н	~		-	Н	H	Н	Н	Н	-	-	Н	н
& Ouery Match Length DB	736	879	187	442	1157	307	1692	1992	199	624	1477	702	878	256	380	400	652	1690	1758	1763	134	180
Query Match	35.4	35.4	34.9	34.9	34.9	33.9	33.9	33.9	33.3	33.3	33.3	32.8	32.8	32.3	32.3	32.3	32.3	32.3	32.3	32.3	31.8	31.8
Score	89	9 6		67	67	65	65	65	64	64	64	63	63	62	62	62	62	62	62	62	61	61
Result No.	н (~ ~	4	ហ	ø	7	00	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

11.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1	
TRANSCRIPTIONAL REGULA HYPOTHETICAL OXIDOREDU HYPOTHETICAL 28 KD PRO COAT PROTHETICAL 28 KD PRO COAT PROTHEIN VP1. BETA-ARRESTIN 2. BETA-ARRESTIN 2. BEGTA-ARRESTIN 2. BEGTA-ARRESTIN 2. LEGUMIN PRECURSOR (BET PRESONNE B ALPHA 2 RE PROBABLE DNA PACKAGING INTERCORSON (BET PROBABLE DNA PACKAGING INTERCORSON LA SAMENTAL A S. S. KD P BETA-ARRESTIN 2. COLLAGEN ALPHA 1(VIII) ACONITATE HYDRATASE, M REGULAGEN ALPHA 1(XII) COLLAGEN ALPHA 1(XII) C	
BASR_SALTY YDGB_ECOLI YPER_HUMAN YPER_HUMAN ARRZ_HUMAN ARRZ_HUMAN ARRZ_HOYIN ULBB_HCKYNA ULBB_HCKYNA ULBB_TCKYNA ULBB_TCKYNA ILITI_HUMAN ILITI_HUMAN ILITI_HUMAN ARRZ_RAT ARRZ_RAT ARRZ_RAT ARRZ_RAT ACON_BOVIN ACON_BOVIN HUSI_COCCA	
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ALIGNMENTS

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879 AA. PRT; RESULT 2 ID YDBH_ECOLI STANDARD; AC P52645; P77502; P76855; ö

Gaps

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P18183;

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HRDB.

RESULT 1D HF DT 011 DT

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-i- FUNCTION: NEMATODE CUTICLES ARE COMPOSED LARGELY OF COLLAGEN-LIKE PROPEINS. THE CUTICLE FUNCTIONS BOTH AS AN EXOSKELETON AND AS A BARKIER TO PROTECT THE WORM FROM ITS ENVIRONMENT.
-i- SUBGNIT: COLLAGEN POLYPEPTIDE CHAINS ARE COMPLEXED WITHIN THE CUTICLE BY DISULFIDE BONDS AND OTHER TYPES OF COVALENT CROSS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYAR_SCHPO STANDARD; PRT; 1692 AA.
P14605;
01-APR-1990 (REL. 14, CREATED)
01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).
CYRL.
                                                                                                                                                                                                                                                                                                                                                                         CAENORHABDITIS ELEGANS.
EUKARYOTA: METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT; MULTIGENE FAMILY; COLLAGEN.
TRIPLE-HELICAL REGION.
TRIPLE-HELICAL REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SIMILARITY: TO OTHER COLLAGENS. STRONG, TO OTHER CUTICLE COLLAGENS. L15418, G289662; -. EMBL; U15418; G289662; -. EMBL; U14635; G540271; ALT_INIT.
                                                                                Score 67; DB 1; Length 1157;
Pred. No. 2.09e+00;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAULEY A.;
SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRIPLE-HELICAL REGION.
TRIPLE-HELICAL REGION.
TRIPLE-HELICAL REGION.
TRIPLE-HELICAL REGION.
                                                 MW; 3FBC3905 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 4.39e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9346DA48 CRC32;
                                                                                                                                                                                                                                                                                     01-FEB-1994 (REL. 28, CREATED)
01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
CUTICLE COLLAGEN 36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
               (POTENTIAL)
                                 (POTENTIAL)
                                                                                                                                                                                                                                                         307 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 65;
                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30126 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WORMPEP; C27H5.5; CE06893.
CUTICLE; CONNECTIVE TISSUE;
                                                 126984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33.98;
55.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214 PGPPGPAGQPGRVIQVNG 231
                                                                              34.9%;
Similarity 60.0%;
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 PGPPGLQGRLQRLLQANG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10; Conservative
                                                                                                                                                     1072 KLEHLYQGNGNHAEG 1086
                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                        KRAMER J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-BRISTOL N2;
MEDLINE; 94131298.
LEVY A.D., KRAMER J.M.;
GENE 137:281-285(1993).
               530
              523 53
840 84
1157 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       260
307 AA;
                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                           COL-36 OR C27H5
                                                                                                                                                                                                                                                       CC36_CAEEL
P34803;
              NP_BIND
NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                       STRAIN-A3(2);
MEDLINE; 89058616.
TANAKA K., SHIINA T., TAKAHASHI H.;
SCIENCE 242:1040-1042(1988).
-!- FUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES
ATTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HEYMAN J.A., MONOSOV E., SUBRAMANI S.;
J. CELL BIOL. 127:1259-1273(1994).
-!- FUNCTION: INVOLVED IN PEROXISOME BIOSYNTHESIS. MAY PLAY A DIRECT OR INDIRECT ROLE IN DELIVERING MEMBRANE MATERIAL TO DEVELOFING PEROXISOMES. IT MAY ALSO BE INVOLVED IN INTRACELLULAR MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X52983; G48745; -.
PIR; 511712; 511712.
PROSITE; PS00715; SIGMA70_1; 1.
PROSITE; PS00716; SIGMA70_2; 1.
TRANSCRIPTION REGULATION; SIGMA FACTOR; DNA-DIRECTED RNA POLYMERASE;
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             233 246 POLYMERASE CORE BINDING (POTENTIAL).
403 422 H-T-H MOTIF (BY SIMILARITY).
442 AA; 48413 MW; 4720321F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           THEN IS RELEASED.
-!- SIMILARITY: TO OTHER SIGMA FACTORS THAT DO NOT BELONG TO THE SIGMA-54 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                 ô
                                                                                                                                                                                                                                                                                                          PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; STREPTOMYCETACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
-!- SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.
EMBL; Z36987; G537420; -.
PROSITE; PS00674; AAA; 1.
Pred. No. 2.09e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
PEROXISOME BIOSYNTHESIS PROTEIN PASI (PEROXIN-1).
PEXI OR PASI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 67; DB 1; LA Pred. No. 2.09e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                      01-NOV-1990 (REL. 16, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1157 AA.
                                                                                                                                                                        442 AA
                                                                                                                                                                                                                                                       RNA POLYMERASE PRINCIPAL SIGMA FACTOR HRDB
                                                                  30 PAGPSIEVKVQQLDPANGNKDVGTVTI 56
                                                                                                  1 PGPPGLQGRLQRLLQANGNHAAGILTM 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEROXISOME; ATP-BINDING; REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  370 LQEQLHSVLDTLSEREAGVVSM 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 LOGRLORLLOANGNHAAGILTM 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.9%;
ilarity 31.8%;
Conservative
               Best Local Similarity 37.0%;
Matches 10; Conservative
                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                          STREPTOMYCES COELICOLOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PICHIA PASTORIS (YEAST)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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MEDLINE; 95050987
                                                                                                                                                   LT 5
HRDB_STRCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOVEMENT
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P46463;
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SEQUENCE
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Matches

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Gaps

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Matches

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RESULT

SCSGEPTERS

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STRAIN-K12 / MG1655;
STRAIN-K12 / MG1655;
STRAIN-K12 / MG1655;
STRAIN-K12 / MG1655;
BLAITNER F.R., PLUNKETT G. III, MAYHEW G.F., PERNA N.T., GLASNER F.D.;
SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- SIMILARITY: TO B.SUBTILIS YWBD.
-!- SIMILARITY: TO B.SUBTILIS YWBD.
-!- SIMILARITY: BELONGS TO THE UPF0020 FAMILY.
EMBL, AE000197; G1787181;
--- ECOGENE; EG13777; YCBY.
PROSITE; PS010261; UPF0020; 1.
PROSITE; PS01092: NG_MTASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESCHERICHIA COLI.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
VOLCKAERT G., VOET M., ROBBEN J.;
YEAST 13:251-259(1997).
-!- FUNCTION: REQUIRED FOR OLIGOMYCIN RESISTANCE.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- SINCLARIAR LOCATION: INTEGRAL MEMBRANE PROTEIN FAMILY
-!- SIMILARITY: BELONGS TO THE APP-BINDING TRANSPORT PROTEIN FAMILY
EMBL, 273066, E243252; --
SCD; LO003083; YOR1.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
ATP-BINDING; TRANSMEMBRANE; GLYCOPROTEIN; TRANSPORT.
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--- ANAWEM 207 227 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
HYPOTHEFICAL 78-9 KD PROTEIN IN PYRD-PQIA INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 64; DB 1; Length 1477;
Pred. No. 6.32e+00;
5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
W; 79B302B8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 63; DB 1; Le
Pred. No. 9.05e+00;
3; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             702 AA; 78854 MW; 3218A412 CRC32;
                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         702 AA
                                                                                                                                                                                                                                                                                      POTENTIAL.
POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     166727 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                499 GRLQSLLEAPEDDPNQMIEM 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 GRLQRLLQANGNHAAGILTM 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32.8%;
larity 61.5%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 33.3%;
Best Local Similarity 40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                          636
913
961
1048
1162
1162
628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROKARYOTA; GRACIL]
ENTEROBACTERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LT 13
YCBY_ECOLI
P75864;
                                                                                                                                                                                                                                                                                                                                                                    NP_BIND
CARBOHYD
                                                                                                                                                                                                                              TRANSMEM
TRANSMEM
TRANSMEM
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                    NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                               MEDILINE; 93449955.

MEDILINE; 93449955.

MEDILINE; 93449955.

L. SIGNELMANN G., KLAUSMEIER P., SCHWENN J.D.;

BIOCHIM. BIOPHYS. ACTA 1144:102-106(1993).

- !- CATALYTIC ACTIVITY: H(2)S + 3 OXIDIZED FERREDOXIN + 3 H(2)O -

SULFITE + 3 REDUCED FERREDOXIN.

- !- COFACTOR: THIS EXZYME CONTAINS ONE SIROHEME AND ONE 4FE-4S

- IRON-SULFUR CENTER AS PROSTHETIC GROUPS.

- IS SUBDINIT: MONOMER:

- SINILARITY: THE C-TERMINAL DOMAIN IS A 4FE-4S/SIROHEME DOMAIN

- FOUND IN NITRITE REDUCTASES (EC 1.6.6.4 AND EC 1.7.7.1) AND

R EMBL; 211755; G38930; - ROLFICE REDUCTASES

R PIR; S19860; RDYCS7.
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 96069397.
KATZMANN D.J., HALLSTROM T.C., VOET M., WYSOCK W., GOLIN J., VOLCKAERT G., MOYE-ROWLEY W.S.;
MOL. CELL. BIOL. 15:6875-6883(1995).
                                                                                                                                                                                                                                                                          SYNECHOCOCCUS SP. (STRAIN PCC 7942) (ANACYSTIS NIDULANS R2) PROKARYOTA; GRACILICUTES; OXYPHOTOBACTERIA;
            DB 1; Length 199;
6.32e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 64; DB 1; Length 624; Pred. No. 6.32e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
0LIGOMYCIN RESISTANCE ATP-DEPENDENT PERMEASE YORI.
                                                                                                                                                                                                                                                                                        PROKARYOTA; GRACILICUTES; OXYPHOYUBALIBAIA;
CYANOBACTERIA (BLUE-GREEN ALGAE); CHROOCOCCALES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                01-APR-1993 (REL. 25, CREATED)
01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
10-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
SULFITE REDUCTASE (FERREDOXIN) (EC 1.8.7.1).
                                            4; Mismatches
                                                                                                                                                                   624 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1477 AA
              Score 64;
Pred. No.
                                                                                                                                                                   PRT;
           33.3%;
Similarity 53.3%;
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.3%;
Similarity 53.3%;
8; Conservative
                                                                          124 PELGALQARLERLLR 138
                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   464 PGLLVRIRRLLEEQG 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                      1 PGPPGLQGRLQRLLQ 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||| |::|||: |
PGLQGRLQRLLQANG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-S288C / FY1679;
MEDLINE; 97245295.
           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                              01-APR-1993 (REL. 01-APR-1993 (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YOR1_YEAST
P53049;
                                                                                                                                                                  SIR_SYNP7
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4

RESULT

Matches

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Gaps

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Gaps

; 0

Length 702; Indels

*****	(TM)
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*****	<u>'</u>

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm Thu Jul 30 09:24:28 1998; MasPar time 5.15 Seconds 220.864 Million cell updates/sec MPsrch_pp : uo d

abular output not generated.

>US-08-938-548A-9 (1-27) from US08938548A.pep 192 1 PGPPGLQGRLORLLQANGNHAAGILTM 27

Title: Description: Perfect Score: Sequence:

Scoring table:

PAM 150 Gap 15

140542 seqs, 42109429 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

sptrembl5
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 29.753; Variance 52.286; scale 0.569

Statistics:

SUMMARIES

Pred. No.	3.48e-01	7.16e-01	4.15e+00	5.84e+00	5.84e+00	5.84e+00	5.84e+00	5.84e+00	5.84e+00	5.84e+00	5.84e+00	8.20e+00	8.20e+00	8.20e+00	8.20e+00	8.20e+00	8.20e+00	8.20e+00	1.15e+01	1.15e+01
Description	PAR INTERACTING PROTEI	K+ CHANNEL BETA4 SUBUN	TIGHT JUNCTION PROTEIN	YONC PROTEIN.	RNA POLYMERASE SIGMA F	ARTICULIN P60.	DNA POLYMERASE III TAU	HRPG.	DEOXYCYTIDINE-TRIPHOSP	UNKNOWN GENE.	T24D5.1.	RNA-DIRECTED DNA POLYM	CARA.	H06001.2.	RETINOID X RECEPTOR IN	P160 MYB-BINDING PROTE				
ΩI	035821	P97382	295168	031955	P95644	059913	P77951	059813	059814	027212	045998	060245	027642	054224	922732	005804	050983	017909	060811	035851
82	10	10	4	σ	σ	σ	σ	σ	σ	m	თ	თ	σ	σ	ო	σ	σ	m	20	10
Length DB	1277	249	1174	178	462	510	514	525	528	268	909	130	150	253	304	319	377	1465	580	1344
Query Match	39.1	38.0	35.4	34.9	34.9	34.9	34.9	34.9	34.9	34.9	34.9	34.4	34.4	34.4	34.4	34.4	34.4	34.4	33.9	33.9
Score	75	73	68	29	67	29	67	49	67	67	67	99	99	99	99	99	99	99	65	65
Result No.	1	7	٣	4	'n	ø	7	80	თ	10	11	12	13	14	15	16	17	18	19	20

1.15e+01 1.60e+01	1.60e+01	1.60e+01	1.60e+01	1.60e+01	1.60e+01	2.22e+01	2.22e+01	2.22e+01	2.22e+01	2.22e+01	3.08e+01	3.08e+01	3.08e+01	3.08e+01	3.08e+01	3.08e+01	3.08e+01	3.08e+01	3.08e+01	3.08e+01	3.08e+01	4.24e+01	4.24e+01
FATTY ACID SYNTHASE (E PUTATIVE SIGMA-54 DEPE	ORF263.	HOMODA HYDROLASE.	ORF328 (FRAGMENT).	PROTEIN-TYROSINE PHOSP	KM-102-DERIVED REDUCTA	HRPE.	FROM BASES 1860594 TO	NODO.	HYPOTHETICAL 85.5 KD P	KIAA0310.	PSSA (FRAGMENT).	METHYLTRANSFERASE.	HYPOTHETICAL 37.6 KD P	F14D7.2.	RNA POLYMERASE SIGMA F	C-SRC TYROSINE KINASE.	RNA POLYMERASE SIGMA F	TYPE VII COLLAGEN (FRA	COLLAGEN A1 XIX CHAIN.	CODED FOR BY C. ELEGAN	C. ELEGANS COLLAGEN AL	RETINA SPECIFIC RGS PR	TRANSCRIPTIONAL ACTIVA
Q16702 Q50872	031722	051980	053921	027932	099475	052495	P76237	007309	P73339	015027	P96282	032855	P74570	019452	059552	091952	059532	063870	035053	019098	019099	P79348	051454
00	9	σ	σ	m	~	σ	σ	σ	σ	~	σ	0	6	ო	σ	12	0	2	2	m	٣	4	σ
2509 140	263	288	294	548	549	439	556	633	770	881	285	310	331	457	466	527	574	920	1136	1758	1759	374	473
33.9	33.3	33.3	33.3	33.3	33.3	32.8	32.8	32.8	32.8	32.8	32.3	32.3	32.3	32.3	32.3	32.3	32.3	32.3	32.3	32.3	32.3	31.8	31.8
65	64	64	64	64	64	63	63	63	63	63	62	62	62	62	62	62	62	62	62	62	62	61	61
21	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

* •		Gaps	
MINARY; PRT; 1277 AA. EEL. 05, CREATED) EEL. 05, LAST SEQUENCE UPDATE) EEL. 05, LAST ANNOTATION UPDATE) EEL. 07, LAST ANNOTATION UPDATE) AT). CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	SCHIBLER U.; EMBL/GENBANK/DDBJ DATA BANKS. - 675 MW; 89721F79 CRC32;	e 75; DB 10; Length 1277; . No. 3.48e-01; Mismatches 5; Indels 0; 852	MINARY; PRT; 249 AA. EL. 03, CREATED) EL. 03, LAST SEQUENCE UPDATE) EL. 03, LAST ANNOTATION UPDATE) UNIT. CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
ID 035821 PRELIMINARY; C 035821 PRELIMINARY; DT 035821 PRELIMINARY; DT 01-JAN-1998 (TREMBLREL. 05, DT 01-JAN-1998 (TREMBLARY) DT 01	SEQUENCE FROM N.A. MEDLINE; 91084634. WUARIN J., SCHIBLER U.; CELL 63:1257-1266(1990). [2] SEQUENCE FROM N.A. COMTE P.A., OSSIPOW V., SCHIBLE SUBMITTED (JUL-1997) TO EMBL/GE EMBL; U83590; G2253211; SEQUENCE 1277 AA; 144675 MW;	Query Match Best Local Similarity 29.6%; Pred Matches 8; Conservative 14; 826 FGAEALHAQVERFVQQAGNQADASVAL 1 PGPPGLQGRLQRLLQANGNHAAGILITM	RESULT 2 P97382 POT 382 POT 38
REPUBLICANT OF THE PROPERTY OF	RA RY	O O O O	RES DT TD DT CO OC CO OC CO RN RP RC

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RESULT

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MEDLINE; 93083996.

KORMANEC J., FARKASOVSKY M., POTUCKOVA L.;
GENE 122:63-70(1992).

-1- FUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES
ATTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES AND
THEN IS RELEASED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M90411; G153306; -.
PROSITE; PS00715; SIGMA70_1; 1.
PROSITE; PS00716; SIGMA70_2; 1.
TRANSCRIPTION REGULATION; SIGMA FACTOR; DNA-DIRECTED RNA POLYMERASE;
                                                                                                                                                                                                                                                                                                                                   PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; STREPTOMYCETACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; STREPTOMYCETACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 67; DB 9; Length 528;
Pred. No. 5.84e+00;
9; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                         CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 67; DB 9; LA
Pred. No. 5.84e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             525 AA; 57204 MW; 7B7689F1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     568 AA.
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                                                              525 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          528
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Q27212 PRELIMINARY; PRT;
Q27212;
01-NOV-1996 (TREMBLREL. 01, CREATED)
                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score Pred. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   453 LQEQLHSVLDTLSEREAGVVSM 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               456 LQEQLQSILGTLSEREAGVVSM 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 LQGRLQRLLQANGNHAAGILTM 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34.9%;
ilarity 31.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TREMBLREL. 01,
01-NOV-1996 (TREMBLREL. 01,
01-JAN-1998 (TREMBLREL. 05,
RNA POLYMERASE SIGMA FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 LOGRLORLLOANGNHAAGILTM
                                                              PRELIMINARY;
                                                                                                                             (TREMBLREL. 01,
(TREMBLREL. 01,
(TREMBLREL. 05,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34.9%;
Similarity 36.4%;
8; Conservative
                                                                                                                                                                                                                                     RNA POLYMERASE SIGMA FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREPTOMYCES AUREOFACIENS
             ULT 8
059813
059813
059813
01-00V-1996 (TREMBLREL. 0
01-00V-1996 (TREMBLREL. 0
01-00V-1998 (TREMBLREL. 0
                                                                                                                                                                                                                                                                                                       STREPTOMYCES AUREOFACIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA-BINDING
SEQUENCE
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ID Q2
AC Q2
DT 01
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                                                              SWEWN READERS OF THE SERVICE OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ά
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENE 153:41-48(1995).

-1- FUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES
ATTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES AND
THEN IS RELEASED.

EMBL: X75922; G581664; -
PROSITE; PS00715; SIGMA70_1; 1.
PROSITE; PS00716; SIGMA70_2; 1.
PROSITE; PS00716; SIGMA FACTOR; DNA-DIRECTED RNA POLYMERASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SHINKAWA H., HATADA Y., OKADA M., KINASHI H., NIMI O.;
SHINKAWA H., HATADA Y., OKADA M., KINASHI H., NIMI O.;
J. BIOCHEM. 118:404-499(1995).
-!- FUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES
ATTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES AND
THEN IS RELEASED.
EMBL, LO8071; G1617256.
-.
PROSITE; PSO0715: SIGMA70_1; 1.
PROSITE; PSO0716; SIGMA70_2; 1.
TRANSCRIPTION REGULATION; SIGMA FACTOR; DNA-DIRECTED RNA POLYMERASE;
DNA-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=IMRU 3570;
MEDLINE: 95189101.
MARCOS A.T., DIEZ B., GUTIERREZ S., FERNANDEZ F.J., OGUIZA J.A.,
MARTIN J.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                    STREPTOMYCES GRISEUS.
PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; STREPTOMYCETACEAE.
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PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; STREPTOMYCETACEAE.
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Pred. No. 5.84e+00;
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Pred. No. 5.84e+00;
11; Mismatches 4; Indels
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01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
RNA POLYMERASE SIGMA FACTOR.
                                                                                                                                                                                                                                                                 01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
RNA POLYMERASE SIGMA FACTOR.
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LQEQLHSVLDTLSEREAGVVAM 411
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6 LQGRLQRLLQANGNHAAGILTM 27
                                      || :|: :|:: || :|::|
LQGRLQRLLQANGNHAAGILTM 27
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6 LQGRLQRLLQANGNHAAGILTM 27
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Best Local Similarity 31.8%;
Matches 7; Conservative
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Best Local Similarity 31.8%;
Matches 7; Conservative
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SEQUENCE
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Q59913
Q59913;
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P77951;
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RESULT

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MEDLINE; 94150718.

MEDLINE; 94150718.

MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., MILSON R., AINSCOOGH R., ANDERSON R., BOWFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A., CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., COULSON A., CRAXTON M., REREIN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISTER N., ACHLAGHAN M., PARSONS J., LLOYD C., MCWURRAY A., MORTIMORE B., O'CALLAGHAN M., PARSONS J., PERCY C., RIFKEN L., SONNHAMMER E., STADEN R., SHOWNERS R., SALLON J., THERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R., WALDAMA P., WEINSTOCK L., VAUDIN M., NATURE 368:32-38(1994).

EMBL: 268012; G1070097; ...

SEQUENCE 304 AA: 34775 MW; C4AALEFB CRC32;
                                                                                                            T24D5.1.
CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
                                                                                                                                                                                    SECUENCE FROM N.A.
WILKINSON J.;
SUBMITTED (NOV-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                      01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 66; DB 3; Le
Pred. No. 8.20e+00;
7; Mismatches 6;
                   304 AA.
                   PRT;
                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 40.9%;
Matches 9; Conservative
RESULT
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Search completed: Thu Jul 30 09:24:41 1998 Job time: 13 secs.

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Length 304; 6; Indels

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Release 3.1A John F. Collins, Biocomputing Research Copyright (c) 1993-1998 University of Edinburgh, U. Distribution rights by Oxford Molecular Ltd

protein · protein database search, using Smith-Waterman algorithm

MPsrch_pp

Thu Jul 30 09:10:49 1998; MasPar time 3.13 Seconds 137.296 Million cell updates/sec .. 0

not generated. lar output

>US-08-938-548A-4 101-28) from USO8938548A.pep 196-11 RSGPPGLOGRLOAGSHHAAGILIM 28 Title: Description: Perfect Score:

Sequence:

PAM 150 Gap 15 Scoring table:

124785 seqs, 15338987 residues

Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

a-geneseq31-2 Database:

| ipart| 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part12 17:part17 18:part18 19:part18 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27

Mean 21.977; Variance 87.361; scale 0.252 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description Pred. No. Retinoid X receptor 1 4.32e+01 Saccharomyces cerevis 5.22e+01 Sylactone synthase OR 5.22e+01 SALV-HA/NUMA fusion prot 5.22e+01 SALV-HA/NUMA fusion prot 5.22e+01 SALFED OR SYNTHAS OR 5.22e+01 SALFANIAN (10) 1.00e+02 Sequence deduced from 1.10e+02 Sequence of human alv 1.10e+02 Sequence of human alv 1.10e+03	
X receptor 1 yese cerevis syces cerevis sytes cerevis sythase OR i fusion prot tumA fusion prot tumA fusion p ces venezuel cerminal (2). eptide based deduced from onary surfac deduced from of human alv iequence of h case	1.10e+02 1.10e+02
Description Retinoid X Saccharomyc S. Saccharomyc S. Tylactone si Sequence de Sequence of Genomic sequence of Human 32K Aulman	Human 32K ASP encoded Plasmid pASPc-SV(10)
DOMESTIC DE LES DOMESTIC DE LE	R04215 P60441
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4.222 + 1.02	248 248
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Nesu No. 100 110 110 110 110 110 110 110 110 11	18 19

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11.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1	1.91e+02 1.91e+02 1.91e+02 1.91e+02 1.91e+02
Vector PSP 35K-1A-10 Human alveolar surfac Human 32K ASP encoded Genomic sequence of h Human 32K alveolar su DHR23alpha protein. Ecdysone receptor. HIV-2 provirus-encode Thermus aquaticus hea Protein (0A-519) cros Human adipogenesis in Human interleukin-11 Human interleukin-11 Sequence of a cytokin Human interleukin-11 Human interleukin-11 Human interleukin-11 Human interleukin-11 Human interleukin-11 Human interleukin-11 Human dipogenesis in Orotidine-5'-monophos Thioredoxin-Il-11 fus E.coli inforedoxin-Il-11	Rat ALT. M. tuberculosis RNA p Virulence-associated Platenolide synthase Platenolide synthase
R05091 R06331 R064217 R04212 R32889 R137889 R137889 R43889 R43283 R43262 R43262 R75337 R75337 R76812 R76812 R76812 R76813 R76812 R76813 R76813 R76813 R76813 R76813 R76813	R35231 W05831 R76480 W22608 W23718
244 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	119 125 25
248 271 271 271 271 169 176 176 177 177 177 177 178 178 178 179 179 179 179 179 179 179 179 179 179	496 528 530 3724 3724
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011222222222222222222222222222222222222	4 4 4 4 4 1 2 6 4 2 2

ALIGNMENTS

Refinoid X receptor (RXR) interacting protein (RIP) - useful to modulate or mediate RXR function, anti-RIP antibodies can be used to determine RIP subcellular distribution patterns
Claim 2, Page 48-50; 90pp; English.

Mouse retinoid X receptor (RXR) interacting protein RIP110 (R99737)
is a candidate transcriptional co-activator. It was identified using an in vivo interaction trap system for the isolation of proteins that physically interact with RXRs, esp. with the ligand binding domain of human RXR alpha. Recombinant RIP110 can be obtd. using a cDNA clone (T31930) obtd. from a mouse liver library. RIPS (see also R99735-36 and R99738-39) can be used to modulate or mediate RXR function, and may be used therapeutically or to raise antibodies. 27-5EP-1996 (first entry)
Retinoid X receptor interacting protein RIP110.
Retinoid X receptor interacting protein; RXR; RIP; RIP110. standard; Protein; 716 AA. 18-JUL-1996. 08-DEC-1995; U16311. 13-JAN-1995; US-372652. (GEMO) GEN HOSPITAL CORP. Chol H, Moore D, Seol W; WPI; 96-342241/34. N-PSDB; T31030. Mus sp. WO9621677-A1. R99737 RESULT

ö Gaps ö 34.7%; Score 68; DB 18; Length 716; 44.4%; Pred. No. 4.32e+01; artive 6; Mismatches 4; Indels Similarity 44.4%; 8; Conservative Query Match Best Local Similarity Matches

621 qgrllslleqsehrttgv 638 |||| || || ::::|: 8 QGRLQRLLQASGNHAAGI 25

g δ

RESULT 2
ID W10424 standard; Protein; 1477 AA.
AC W10424;
W10424;
DT 18-AUG-1997 (first entry)
DE Saccharomyces cerevisiae aureobasidin resistance protien scaur2.

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09-JAN-1992.
27-JUN-1991; U04588.
27-JUN-1990; US-544862.
(BIOG-) BIOGEN INC.
                                                          2272 AA;
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                                                          Sequence
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                                                                                                                                                                                        Claim 15; Page 42-50; 78pp; English.

The sequences given in W21731-32 represent fusion proteins which contain NuMA (nuclear mitotic apparatus). The fusion proteins were used in the identification of NuMA interecting proteins (NIP's) (see also W21729-30). Compounds which interfere with the interaction of NuMA (w21729-30). Compounds which interfere with the interaction of NuMA with the interaction interaction with the interaction interaction with the interaction with the interaction with the interaction of NuMA or NIP which may be markers for aberrant (including malignant) call growth (which can also be detected by nucleic acid sequencing). Also where manignancy is related to defects in NuMA or NIP, it can be treated by administration of the appropriate functional protein.
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The sequences given in W21731-32 represent fusion proteins which contain NuMA (nuclear mitroit apparatus). The fusion proteins were used in the identification of NuMA interecting proteins (NIP's) (see also W21729-30). Compounds which interfere with the interaction of NuMA with a known NIP are used to modulate cell division and/or proliferation. As trained conventionally using NIP-1 or -2 as immunogen, are used to detect NIP (or their complexes) and to block their activity for diagnostic or therapeutic use, e.g. to detect defective NuMA or NIP which may be markers for aberrant (including malignant) cell growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W21731;
01-0CT-1997 (first entry)
6AL4/HA/NuMA fusion protein.
NIP-1; NIP-2; NUMA; nuclear mitotic apparatus; NUMA interacting protein;
cell division; proliferation; antibody; Ab; detection;
malignant cell growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                   New nucleic acid encoding nuclear mitotic appts. Interacting proteins – useful for modulating cell division and proliferation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding nuclear mitotic appts. Interacting proteins – useful for modulating cell division and proliferation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 67; DB 23; Length 2192;
Pred. No. 5.22e+01;
5; Mismatches 3; Indels (
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171abel - Residues_18-2116_of_NuMA
365.1864
/label - Colled_coll_region
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label- GAL4_DNA_binding_domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W21731 standard; Protein; 2272 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34.2%;
larity 52.9%;
Conservative
                                                                        McPherson SMG, Snyder MP;
WPI; 97-077270/07.
N-PSDB; T77783.
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WPI; 97-077270/07.
N-PSDB; T77782.
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07-JUN-1996; U09504.
07-JUN-1995; US-478408.
(UYXA ) UNIV YALE.
                                    US-478408.
                07-JUN-1996; U09504
07-JUN-1995; US-4784
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                                                        (UYYA ) UNIV YALE.
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                                                                                                                                                                            in diagnosis
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Industrial use
Claim 55; Fig 23; 91pp; English.
Solyapetide sequences (W19629-30 and W00918) can be deduced from
3 Polyapetide sequences (W19629-30 and W00918) can be deduced from
5 Streptomyces venezuelae. The sequence data indicate that the PKS
5 Gene cluster encodes a polyene of 12 carbons. The vep gene cluster
5 Gene cluster encodes a polyene of 12 carbons. The vep gene cluster
6 contains 5 PKS modules, plus a 5' loading module and a 3' end
7 contains 5 PKS modules, plus a 5' loading module and a 3' end
8 contains 5 PKS modules, plus a 5' loading module and a 3' end
8 contains 5 PKS modules, plus a 5' loading module and a 3' end
8 a contains 5 PKS modules, plus a 5' loading module and a 3' end
8 a contains 5 PKS modules, and module a keto-ACP, an
8 a contains 6 PKS module and and a contains
8 contains 6 PKS module cluster and module 7 from the Streptomyces
8 tylp gene cluster has polyhydroxyalkanoate (PHA) monomer synthase
8 a biodegradable polymer.
8 cfor use as a biodegradable polymer.
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(which can also be detected by nucleic acid sequencing). Also where malignancy is related to defects in NuMA or NIP, it can be treated by administration of the appropriate functional protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Expression cassettes for production of polyhydroxyalkanoate(s) provide wide range of biodegradable polymers for medical or
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                                                                                                                                                            Length 2272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptomyces venezuelae polyketide synthase.
Polyketide synthase; polyhydroxyalkanoate monomer synthase;
polyhydroxybutyrate; biodegradable polymer; vep gene;
                                                                                                                            Score 67; DB 23; Length 441.
Pred. No. 5.22e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 67; DB 22; Length 463
Pred. No. 5.22e+01;
9; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "polymorphism - see CC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     p33" N-terminal (2).
AP: lymphocyte; IL-2; CTL; polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4302 rdtpaalaahlaellatardhgpg 4325
                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
ID W19629 standard; Protein; 4630 AA.
AC W19629;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xue Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24
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R20235 standard; Protein; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34.2%;
Local Similarity 33.3%;
hes 8; Conservative
                                                                                                                                                         Query Match
Best Local Similarity 52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MINU) UNIV MINNESOTA.
Sherman DH, Williams MD,
WPI; 97-341701/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R20235;
24-APR-1992 (first entry)
                                                                                                                                                                                                                                                                                  918 ragrkglearlqqlgea 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-SEP-1997 (first entry)
                                                                                                                                                                                                                     9; Conservative
                                                                                                                                                                                                                                                                                                                                            1 RSGPPGLQGRLQRLLQA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces venezuelae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-DEC-1996; U20119.
19-DEC-1995; US-008847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              metabolic engineering.
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The sequence was deduced from clone pHS10-4, isolated from a human lung cDNA library. The protein is part of the alveolar surfactant protein, high mol. wt, hydrophilic 32K gp. The protein differs at 7 positions from a previously published (WO8603408) sequence, and also at several places from two other sequences determined by others. It is believed that the 32K human ASP protein may be encoded by multiple genes. The recombinant protein can be used for the treatment of respiratory disorders.
                                                                               Recombinant alveolar surfactant protein – used for treating respiratory distress syndrome and related diseases e.g. pneumonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Regulatable expression systems - contg. human metallo:thionein-II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-JUL-1991 (first entry)
Genomic sequence of human alveolar surfactant protein (hASP)
encoded by genomic DNA, used to obtain pASPcg-SV(10)
Regulatable expression system.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                   Score 63; DB 1; Length 248; Pred. No. 1.10e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example; Fig 5, 94pp; English.

A regulatable expression system for a coding sequence is. The system can process genomic as well as intronless DNA. Sequence 248 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-JUL-1991 (first entry)
Sequence of human alveolar surfactant protein (hASP)
on DWI(E):HS and PASPC-SV(10)
Regulatable expression system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 63; DB 3; L
Pred. No. 1.10e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-FEB-1985; US-701296.
25-NOV-1985; US-8011674.
(KUSH/) BIOTECHN RES PARTNE.
(KUSH/) KUSHNER P J.
Kushner PJ. Cofer CL, Friedman J, Talmadge KD;
N-PSDB; N60571.
                (CALB-) Calif Biotechn Inc.
Schilling JW, White RT, Cordell B, Benson BJ;
                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T 15
P60666 standard; Protein; 248 AA.
P60666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      n 14
P60665 standard; Protein; 248 AA.
P60665;
                                                                                                                                                                                                                                                                                                                                                                                   Query Match 32.1%;
Best Local Similarity 56.3%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 32.1%;
Best Local Similarity 56.3%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95 gppglpahldeelqat 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95 gppglpahldeelqat 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 GPPGLQGRLQRLLQAS 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 GPPGLOGRLORLLOAS 18
                                                                                                                      and bronchitis.
Disclosure; pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-FEB-1986; U00296
                                                                                                                                                                                                                                                                                                                                               248 AA;
                                                          WPI; 88-124493/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
WO8604920-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-AUG-1986
                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      promoter
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                                                                                                                  Disclosure: pp; English.

The sequence was deduced from clone pHS10-5, isolated from a human lung cDNA library. The protein is part of the alveolar surfactant protein, high mol. wt, hydrophilic 32K sp. The protein differs at position 50 from a previously published (WO8603408) sequence, and differs at several places from two other sequences determined by others. It is believed that the 33K human ASP protein may be encoded by multiple genes. The recombinant protein can be used for the treatment of respiratory disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pulmonary surfactant proteins - used for treating Hyaline Membrane
Disease or Respiratory Distress Syndrome.
Claim 1; Page 34A-B; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene product may be used in treatment of Hyaline Membrane Disease
and Respiratory Distress Syndrome (RDS) in both premature infants
and adults eg. cardio-pulmonary operations. The protein products
may also be used to raise diagnostic antibodies.
                                                          Recombinant alveolar surfactant protein – used for treating respiratory distress syndrome and related diseases e.g. pneumonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-DEC-1990 (first entry)
Sequence deduced from PHS10-4, encoding human 32K ASP.
Alveolar surfactant protein; ASP; respiratory distress syndrome;
pneumonia; bronchitis; 32K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P70663;
29-APR-1991 (first entry)
35kd pulmonary surfactant protein.
Hyaline membrane disease; respiratiory distress syndrome; RDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                  Length 248;
                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BRIG-) Brigham and Women's Hospital.
Taeusch HW, Cobs KA, Steinbrink DR, Floros J, Phelps DS;
WPI; 87-108682/15.
                                                                                                                                                                                                                                                                                                                                                                Score 63; DB 1; L/
Pred. No. 1.10e+02;
(CALB-) Calif Biotechn Inc.
Schilling JW, White RT, Cordell B, Benson BJ;
WPI; 88-124493/18.
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P82980 standard; protein; 248 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   I 12
P70663 standard; Protein; 248 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GENE-) Genetics Institute Inc.
                                                                                                                                                                                                                                                                                                                                                                32.1%;
llarity 56.3%;
Conservative
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56.3%;
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26-SEP-1985; US-781130.
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15-JAN-1987; U00092.
                                                                                                                                                                                                                                                                                                                                                                  Query Match
Pest Local Similarity
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Matches 9; Conserv
                                                                                                  and bronchitis.
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                                                                                                                                                                                                                                                                                                                               Seguence
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu Jul 30 09:13:08 1998; MasPar time 1.15 Seconds 142.938 Million cell updates/sec lar output not generated. Run on:

196 1 RSGPPGLOGRLORLLQASGNHAAGILIM 28 >US-08-938-548A-4 (1-28) from US08938548A.pep Description: Perfect Score: Title:

PAM 150 Gap 15 Scoring table:

Sequence:

Searched:

63816 segs, 5850866 residues

Minimum Match 0% Listing first 45 summaries Post-processing:

a-issued 1:5_COMB 2:PCT9_COMB 3:backfiles Database:

Mean 20.276; Variance 81.503; scale 0.249 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

10	н																					
1.336+	1.95e+0	4.17e+0]	4.17e+01	6.07e+01	6.07e+01	6.07e+01	6.07e+01	6.07e+01	6.07e+01	6.07e+01	6.07e+01	6.07e+01	6.07e+01	6.07e+01	6.07e+01	6.07e+01	6.07e+01	7.31e+01	7.31e+01	7.31e+01	7.31e+01	8.79e+01
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	_	PCT-US96-1 S		,	,	,	PCT-US93-0 S	US-08-017- St	US-07-941- S	115-		ļ	,	,	0		_			-445-		US-07-776- S
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716	10	176	2509	199	199	199	199	199	199	296	296	296	296	296	296	296	1271	829	829	829	829	26
34.7	33.7	31.6	31.6	30.6	30.6	30.6	30.6	30.6	30.6	30.6	30.6	30.6	30.6	30.6	30.6	30.6	30.6	30.1	30.1	30.1	30.1	. 29.6
68	99	62	62	9	9	9	9	9		9	9	9	9	9	9	9	9	59	59	. 59	29	28
	7	e	4	S	ø	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23
	2 PCT-US95-1 Sequence 4, Applicatio 1	2 PCT-US95-1 Sequence 4, Applicatio 1. 2 PCT-US91-0 Sequence 3, Applicatio 1.	7 716 2 PCT-US95-1 Sequence 4, Applicatio 1 10 2 PCT-US91-0 Sequence 3, Applicatio 4 5 176 2 PCT-US96-1 Sequence 6, Applicatio 4	7 716 2 PCT-US95-1 Sequence 4, Applicatio 1 1 2 PCT-US91-0 Sequence 3, Applicatio 1 5 176 2 PCT-US96-1 Sequence 6, Applicatio 4 5 2509 1 US-08-469- Sequence 10, Applicati 4	7 716 2 PCT-US95-1 Sequence 4, Applicatio 1 7 10 2 PCT-US91-0 Sequence 3, Applicatio 1 5 176 2 PCT-US96-1 Sequence 6, Applicatio 4 6 2509 1 US-08-469- Sequence 10, Applicatio 4 5 199 1 US-08-792- Sequence 8, Applicatio 6	34.7 716 2 PCT-US95-1 Sequence 4, Applicatio 1 31.7 10 2 PCT-US91-0 Sequence 3, Applicatio 1 31.6 176 2 PCT-US96-1 Sequence 6, Applicatio 4 31.6 2509 1 US-08-469- Sequence 10, Applicatio 6 0.6 199 1 US-08-992- Sequence 8, Applicatio 6 10.9 1 US-07-949- Sequence 4, Applicatio 6 10.0 1 US-07-949- Sequence 2.0 Mapplicatio 6 10.0 1 US-07-949- Sequence 1.0 Mapplicatio 6 10.0 1 US-07-949- Sequence 1.0 Mapplicatio 6 10.0 10.0 Mapplicatio 6 10.0 Mapplica	34.7 716 2 PCT-US95-1 Sequence 4, Applicatio 1 31.7 10 2 PCT-US91-0 Sequence 3, Applicatio 1 31.6 176 2 PCT-US96-1 Sequence 6, Applicatio 4 31.6 2509 1 US-08-469- Sequence 10, Applicatio 6 30.6 199 1 US-07-949- Sequence 8, Applicatio 6 30.6 199 1 US-08-915- Sequence 2, Applicatio 6 30.6 199 1 US-08-115- Sequence 2, Applicatio 6	34.7 716 2 PCT-US95-1 Sequence 4, Applicatio 1 31.7 10 2 PCT-US91-0 Sequence 3, Applicatio 1 31.6 176 2 PCT-US95-1 Sequence 6, Applicatio 4 31.6 2509 1 US-08-469- Sequence 10, Applicatio 4 30.6 199 1 US-08-792- Sequence 8, Applicatio 6 30.6 199 1 US-08-9115- Sequence 4, Applicatio 6 30.6 199 1 US-08-9115- Sequence 2, Applicatio 6 30.6 199 2 PCT-US33-0 Sequence 2, Applicatio 6 30.6 105 PCT-US33-0 Sequence 3, Applicatio 6 30.6 105 PCT-US33-0 PCT-US3-0 PCT-US33-0 PC	34.7 716 2 PCT-US95-1 Sequence 4, Applicatio 1 31.7 10 2 PCT-US91-0 Sequence 3, Applicatio 1 31.6 176 2 PCT-US96-1 Sequence 6, Applicatio 4 31.6 2509 1 US-08469- Sequence 10, Applicatio 4 30.6 199 1 US-08-792- Sequence 8, Applicatio 6 30.6 199 1 US-08-949- Sequence 2, Applicatio 6 30.6 199 1 US-08-115- Sequence 2, Applicatio 6 30.6 199 2 PCT-US93-0 Sequence 2, Applicatio 6 30.6 199 1 US-08-017- Sequence 4, Applicatio 6 30.6 199 1 US-08-017- Sequence 2, Applicatio 6 30.6 199 1 US-08-017- Sequence 3, Applicatio 6 30.6 199 1 US-08-017- Sequence 4, Applicatio 6 30.6 199 1 US-08-017- Sequence 10.5 US-08-017- Sequence 10.5 US-08-017- US-08-08-017- US-08-017- US-08-08-017- US-08-017- US-08-01	34.7 716 2 PCT-US95-1 Sequence 4, Applicatio 1 31.7 10 2 PCT-US95-1 Sequence 4, Applicatio 1 31.6 176 2 PCT-US96-1 Sequence 6, Applicatio 1 31.6 2509 1 US-0876-1 Sequence 10, Applicatio 4 30.6 199 1 US-08-992- Sequence 8, Applicatio 6 30.6 199 1 US-07-949- Sequence 2, Applicatio 6 30.6 199 1 US-08-115- Sequence 2, Applicatio 6 30.6 199 1 US-08-017- Sequence 2, Applicatio 6 30.6 199 1 US-08-017- Sequence 2, Applicatio 6 30.6 199 1 US-08-017- Sequence 2, Applicatio 6 30.6 199 1 US-07-941- Sequence 3, Applicatio 6 30.6 199 1 US-07-941- Sequence 3, Applicatio 6 30.6 199 1 US-07-941- Sequence 3, Applicatio 6 30.6 199 1 US-07-941- Sequence 5, Applicatio 6 30.6 199 1 US-07-941- Seq	34.7 716 2 PCT-US95-1 Sequence 4, Applicatio 1 31.7 10 2 PCT-US91-0 Sequence 3, Applicatio 1 31.6 176 2 PCT-US95-1 Sequence 6, Applicatio 1 30.6 199 1 US-OB-469- Sequence 10, Applicatio 6 30.6 199 1 US-OB-792- Sequence 4, Applicatio 6 30.6 199 1 US-OB-115- Sequence 2, Applicatio 6 30.6 199 1 US-OB-115- Sequence 4, Applicatio 6 30.6 199 1 US-OB-115- Sequence 4, Applicatio 6 30.6 199 1 US-OB-115- Sequence 4, Applicatio 6 30.6 199 1 US-OB-115- Sequence 7, Applicatio 6 30.6 199 1 US-OB-115- Sequence 7, Applicatio 6 30.6 199 1 US-OB-115- Sequence 7, Applicatio 6 30.6 10.5 US-OB-115- Sequence 7, Applicatio 6 30.6	34.7 716 2 PCT-US95-1 Sequence 4, Applicatio 1 31.7 10 2 PCT-US91-0 Sequence 3, Applicatio 1 31.6 176 2 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US-08-115- Sequence 14, Applicatio 6 20.0 1 US-08-115- Sequence	34.7 716 2 PCT-US95-1 Sequence 4, Applicatio 1 31.7 10 2 PCT-US91-0 Sequence 3, Applicatio 1 31.6 176 2 PCT-US96-1 Sequence 6, Applicatio 1 31.6 2509 1 US-08-469- Sequence 10, Applicatio 4 30.6 199 1 US-08-792- Sequence 8, Applicatio 6 30.6 199 1 US-08-99- Sequence 2, Applicatio 6 30.6 199 1 US-08-115- Sequence 2, Applicatio 6 30.6 199 1 US-08-017- Sequence 2, Applicatio 6 30.6 199 1 US-08-017- Sequence 2, Applicatio 6 30.6 199 1 US-08-017- Sequence 2, Applicatio 6 30.6 296 1 US-07-941- Sequence 4, Applicatio 6 30.6 296 1 US-07-745- Sequence 14, Applicatio 6 30.6 296 1 US-07-745- Sequence 14, Applicatio 6 30.6 296 1 US-07-941- Sequence 14, Applicatio 6 296 1 US-07-941- Sequence 24, Applicatio 6 296 200 200 200 200 200 200 200 200 200 20	34.7 716 2 PCT-US95-1 Sequence 4, Applicatio 1 31.7 10 2 PCT-US91-0 Sequence 3, Applicatio 1 31.6 176 2 PCT-US91-0 Sequence 6, Applicatio 1 31.6 2509 1 US-OB-469- Sequence 10, Applicatio 4 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Sequence 6, Applicatio 1 6 2 31.6 2509 1 US-OB-469- Sequence 6, Applicatio 4 6 30.6 199 1 US-OB-792- Sequence 8, Applicatio 6 0 30.6 199 1 US-OB-794- Sequence 2, Applicatio 6 0 30.6 199 1 US-OB-115- Sequence 2, Applicatio 6 0 30.6 199 1 US-OB-115- Sequence 2, Applicatio 6 0 30.6 199 1 US-OB-115- Sequence 2, Applicatio 6 0 30.6 296 1 US-OB-115- Sequence 1, Applicatio 6 0 30.6 296 1 US-OB-115- Sequence 14, Applicatio 6 0 30.6 296 1 US-OP-941- Sequence 14, Applicatio 6 0 30.6 296 1 US-OP-941- Sequence 14, Applicatio 6 0 30.6 296 1 US-OP-941- Sequence 14, Applicatio 6 0 30.6 296 1 US-OP-941- Sequence 14, Applicatio 6 0 30.6 296 1 US-OP-921- Sequence 14, Applicatio 6 0 30.6 296 2 PCT-US93-0 Sequence 14, Applicatio 6 0 30.6 296 2 PCT-US93-0 Sequence 14, Applicatio 6 10 30.6 296 2 PCT-US93-0 Sequence 14, Applicatio 6 10 30.6 296 2 PCT-US93-0 Sequence 14, Applicatio 6 296 296 2 PCT-US93-0 Sequence 14, Applicatio 6 296 296 2 PCT-US93-0 Sequence 24, Applicatio 6 296 296 2 PCT-US93-0 Sequence 24, Applicatio 6 296 2 PCT-US94-0 PC	68 34.7 716 2 PCT-US95-1 Sequence 4, Applicatio 1 6 33.7 10 2 PCT-US91-0 Sequence 3, Applicatio 1 6 2 31.6 176 2 PCT-US91-0 Sequence 6, Applicatio 1 6 2 31.6 2509 1 US-OB-469- Sequence 10, Applicatio 4 6 30.6 199 1 US-OB-499- Sequence 10, Applicatio 6 0 30.6 199 1 US-OB-999- Sequence 2, Applicatio 6 0 30.6 199 2 PCT-US93-0 Sequence 2, Applicatio 6 0 30.6 199 1 US-OB-115- Sequence 2, Applicatio 6 0 30.6 199 1 US-OB-115- Sequence 3, Applicatio 6 0 30.6 296 1 US-OB-15- Sequence 4, Applicatio 6 0 30.6 296 1 US-OB-15- Sequence 14, Applicatio 6 0 30.6 296 1 US-OP-941- Sequence 14, Applicatio 6 0 30.6 296 1 US-OP-941- Sequence 14, Applicatio 6 0 30.6 296 1 US-OP-921- Sequence 14, Applicatio 6 0 30.6 296 1 US-OP-921- Sequence 14, Applicatio 6 0 30.6 296 1 US-OP-921- Sequence 14, Applicatio 6 0 30.6 296 2 PCT-US93-0 Sequence 14, Applicatio 6 0 30.6 296 2 PCT-US93-0 Sequence 14, Applicatio 6 0 30.6 296 2 PCT-US94-1 Sequence 14, Applicatio 6 0 30.6 296 2 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	25	28	σ,	27	Ч	US-08-062-	7	۲.
	26	28	σ.	199	m	5215895-3	•	.79
	27	28	6	199	m	5215895-4	ö	8.79
	28	28	σ.	199	ч	US-07-949-	7	ω
	29	28	6	199	П	US-08-017-	7	œ
	30	28	6	302	П	US-07-783-	Н	ω
	31	28	6	351	~	PCT-US91-0	Н	œ
	32	28	6	526	П	US-08-298-	equence 4	
	33	28	6	$^{\circ}$	~	US-08-026-	m	œ
	34	22	σ.	œ	Н	US-08-188-	equence 1	Н
	35	22	6	œ	Н	US-08-646-	Ä	Н
	36	57	σ.	œ	Н	US-08-646-	H	÷.
	37	27	φ.	œ	Н	US-08-188-	H	H
	38	22	29.1	2101	Н	US-08-470-	4	H
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						ALIGNMENTS		
RESULT ID P	JLT PCT-(1 7S95-1	T PCT-US95-16311-4	ST	ARD	STANDARD; PRT	; 716 AA.	
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APPLICANT: MOOIE, David
APPLICANT: Seol, Wongi
SAPLICANT: Choi, Hueng-Sik
IITLE OF INVENTION: RETINOID X RECEPTOR-INTERACTING
TITLE OF INVENTION: POLYPEPTIDES AND RELATED MOLECULES AND METHODS
CORRESPONDENCE 17 Sequence 4, Application PC/TUS9516311 GENERAL INFORMATION: Sequence 4, Application PC/TUS9516311

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16311
FILING DATE: ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street, Suite 3100 CITY: Boston STATE: MA COUNTRY: USA ZIP: 02110-2804

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/372,652
FILING DATE: 13-JAN-1995
ATTORNEY AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE DOCKET NUMBER: 00786/246001
TELEPHONE: 617/542-5070
TELEPHONE: 617/542-8906
TELEPAX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:

LENGIH: 716 amino acids TYPE: amino acid

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                                                                                               Length 199;
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Patent No. 5700664
GENERAL INFORMATION:
APPLICANT: Yang, Yu-chung
APPLICANT: Bennett, Frances
TITLE OF INVENTION: A MAMMALIAN CYTOKINE, IL-11
NUMBERSONDENCE ADDRESS:
ADDRESSEE: LEGAL AFFAIRS
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/07/949,516A
FILING DATE: 19-NOV-1992
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        199 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 60; DB 1; L
Pred. No. 6.07e+01;
3; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: -21..0
SEQUENCE 199 AA; 21429 MW; 188641 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/07949516A
                                                                       E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70.6%; Iocal Similarity 70.0%; Pess 7; Conservative
                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein
                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
   THOUSAND OAKS
                                                                                       COMPUTER: IBM PC of OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Protein
LOCATION: 1..178
                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Region LOCATION: -21..0
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ZIP: 02140
                                           91320
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                               COUNTRY:
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Patent No. 5741772
GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: 1840 DEHAVILLAND DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31.6%; Score 62; DB 1; Lent
larity 32.0%; Pred. No. 4.17e+01;
Conservative 9; Mismatches 8;
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TITLE OF INVENTION: CANCER RELATED ANTIGEN
          NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BAKER & BOTTS, L.L.P.
STREET: 1299 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASLSEO Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,005A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 536
FILING DATE: 24-JAN-1994
APPLICATION NUMBER: 08/188,426
FILING DATE: 24-JAN-1994
APPLICATION NUMBER: 08/096,908
FILING DATE: 26-JUL-1993
APPLICATION NUMBER: 07/917,716
FILING DATE: 24-JUL-1992
ATOMNEY/AGENT INFORMATION:
NAME: POSOTSKE, LAULENCE H
REGISTRATION NUMBER: 34,694
                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 062482-0113
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-639-7700
TELEFAX: 202-639-7890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AL SOURCE:
2509 AA; 273089 MW; 32011381 CN;
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INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 2509 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                     COUNTRY: USA
ZIP: 20004-2400
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FRAGMENT TYPE:
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Patent No. 5460810
GENERAL INFORMATION:
APPLICANT: Williams, David A.
APPLICANT: Williams, David A.
APPLICANT: Clark, Steven C.
TITLE OF INVENTION: Method of Treating Cell Damage or TITLE OF INVENTION: Depletion
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSEE: ADDRESSEE: Spring House Corporate Center no new contraction of the contracti
                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: BENNETT, FRANCES K
APPLICANT: PAUL, STEPHAN R
APPLICANT: PAUL, STEPHAN R
APPLICANT: TANG, VU-CHUNG
TILLE OF INVENTION: A MAMMALIAN CYTOKINE, IL-11
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LEGAL AFFAIRS - GENETICS INSTITUTE, INC.
STREET: 87 CAMBRIDGEPARK DRIVE
CITY: CAMBRIDGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 60; DB 1; Length 199;
Pred. No. 6.07e+01;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: GI 5174A-DIV TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 876-1210 X8574 TELEPHONE: (617) 876-5851 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
SEQUENCE 199 AA; 21429 MW; 188641 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                         Sequence 4, Application US/08017522A
Patent No. 5371193
                                                       Sequence 4, Application US/08017522A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/07941372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: MEINERT, M C
REGISTRATION NUMBER: 31,544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 199 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
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Similarity 70.0%;
7; Conservative
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Best Local Similarity
Matches 7; Conserv
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7 LQGRLQRLLQ 16
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ZIP: 02140
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US-07-941-372-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
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APPLICANT: Clark, Steven C.
TITLE OF INVENTION: Method of Treating Cell Damage or
TITLE OF INVENTION: Depletion
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWSON and HOWSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 60; DB 1; Length 199;
Pred. No. 6.07e+01;
'''....*rhes 0; Indels
                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/941,372
FILING DATE: 19920902
CLASSIFICATION: 424
ATONNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REGISTRATION NUMBER: INDUSI
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-9206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spring House Corporate Cntr, P.O. Box 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/115,680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       296 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
JENCE 199 AA; 21429 MW; 188641 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                             COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 119477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 199 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Spring House
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative
Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                    USA
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                                    19477
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US-08-115-680-4
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                    COUNTRY:
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FILING DATE:

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OURTRIAND SISTEM: PC_LOUS/MAJ-DUS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/921,848
FILING DATE: 19920728
FLING DATE: 19920728
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/652,531
FILING DATE: 06-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,382
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: CSerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: 31,822
REFERENCE/DOCKET NUMBER: G15188A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: 617,876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 60; DB 1; L
Pred. No. 6.07e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
ADDRESSEE: Genetics Institute, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 296 AA; 31769 MW; 414378 CN;
                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: Thu Jul 30 09:13:14 1998 Job time: 6 secs.
                     STREET: 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (617) 876-11:
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 296 amino acids
AMINO ACID
                                                                    Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 30.6%;
Best Local Similarity 70.0%;
Matches 7; Conservative
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                                                                                              U.S.A.
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                                                                                                                 ZIP: 02140
                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                               PEPTIDE AND PROTEIN FUSIONS TO THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED THIOREDOXIN-LIKE MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 14, Application US/07921848
Patent No. 5292646
GENERAL INFORMATION:
APPLICANT: McCOy, John
APPLICANT: LaVallie, Edward
TITLE OF INVENTION: Peptide and Protein Fusions To
TITLE OF INVENTION: Thioredoxin and Thioredoxin-Like Molecules
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                        STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
21P: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTING TREBASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/165,301A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  296 AA
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Pred. No. 6.07e+01;
                                                                                                                                                       APPLICANT: MCCOY, John
APPLICANT: DiBlasio-Smith, Elizabeth
APPLICANT: Grant, Kathheen
APPLICANT: Grant, Kathheen
APPLICANT: LaVallie, Edward R.
TITLE OF INVENTION: THIOREDOXIN, THIORE
ITILE OF INVENTION: THIOREDOXIN-LIKE MC
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                   E: Genetics Institute, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Meinert, M. C.
REGISTATION NUMBER: 33,544
REFERENCE/DOCKET NUMBER: GI 5188D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
SEQUENCE 296 AA; 31769 MW; 414378 CN;
                                                                                            Application US/08165301A
                                               Sequence 14, Application US/08165301A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14, Application US/07921848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPRONE: (617) 876-1170
TELERAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 296 amino acids
amino acid
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Similarity 70.0%;
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                                                                                                               Patent No. 5646016
GENERAL INFORMATION:
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US-07-921-848-14
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Length 296; 0; Indels

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu Jul 30 09:08:48 1998; MasPar time 5.39 Seconds 257.683 Million cell updates/sec llar output not generated. : CO

>US-08-938-548A-3 (1-33) from US08938548A.pep 256 1 OPLPDCCROKTCSCRLYELLHGAGNHAAGILTL.33 Title:

Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

140542 segs, 42109429 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

sptrembl5
1:sp_fung1 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Mean 30.295; Variance 46.908; scale 0.646 Statistics:

SUMMARIES

ID Description
002839
022187
24453
001938
224209
261639
33367
001969
291493
248791
248712
290975
P94426
028584
013388
001473
P75863
244258
018373

8.38e+00	1,216+01	1.21e+01	1.21e+01	1.21e+01	1.21e+01	1.21e+01	1.21e+01	1.21e+01	1.21e+01	1.21e+01	1.21e+01	1.73e+01	1.73e+01	1.73e+01	1.73e+01	1.73e+01	1.73e+01	1.73e+01	1.73e+01	1.73e+01	1.73e+01	2.47e+01	2.47e+01
SELENOPHOSPHATE SYNTHE	COSMID C27A2	RIBONUCLEASE.	T21B10.6.	F21C3.1.	AMINO ACID TRANSPORTER	TETRACYCLINE RESISTANC	TETRACYLINE RESISTANCE	ORF11.	TETM GENE.	LET 858.	SIMILARITY TO EGF-LIKE	NONMUSCLE MYOSIN HEAVY	NONMUSCLE MYOSIN HEAVY	NONMUSCLE MYOSIN HEAVY	DNA FOR DNAJ, COMPLETE	NONMUSCLE MYOSIN HEAVY	NONMUSCLE MYOSIN HEAVY	T24D5.1.	N-METHYL-D-ASPARTATE R	N-METHYL-D-ASPARTATE R	N-METHYL-D-ASPARTATE R	TRKB (FRAGMENT).	MYOSIN HEAVY CHAIN, NO
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018597	018238	004393	022627	019671	039135	053770	967709	057224	047810	017336	018857	027991	012989	927990	033700	062707	962706	922732	912879	Q63728	008948	091373	002015
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25	2 4	24	24	24.	24.	24	24	24	77	24	24	24	24	24	24	24	24	24	24	24	24	23	23
64	9 6	63	63	63	63	63	63	63	63	63	63	62	62	62	62	. 62		62	62	62	62	61	61
21	3 6	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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					(E)			EUKARYOTA; META2OA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;					TOYOMURA K., FUJIMURA I., MURAKAMI H., NATSUME I., SHIGEHISA I.,						Score 77; DB 4; Length 363;		Indels			
	Y			01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)	N UPDAT			TETRAPC					SUME I.					(C32;	4; Ler	e-02;	6			
	363 AA.			NCE	ATIC			TA;					NAT					A CR	DB	5.22	tche			
	m		â	EQUE	IONN			EBRA					н.,					4F57	77;	Q	isma	124		53
	PRT;		(TREMBLREL. 04, CREATED)	LAST S	LAST A	PORCINE MEMBRANE COFACTOR PROTEIN.		A; VERT					IRAKAMI	TA T.;	<pre>INT. IMMUNOL. 9:869-876(1997).</pre>			363 AA; 39692 MW; AD14F57A CRC32;	Score	Pred. No. 5.22e-02;	7; Mismatches	98 PLQEACRRKACS-NLPDPLNGQVSYPNG 124	 	PLPDCCRQKTCSCRLYELLHGAGNHAAG 29
	ARY;		04,	04,	05,	OR PF		RDATA					¥ :	NOSHI	(1997			32 MV		36;	ē	CNGQ	-	HGAC
	IMI NZ		REL.	ÆL.	REL.	PACTO		CHO	TLA.				E AS	, KI	918-	989;		3968	30.	39	ztir	CPDPI		XEL
	PRELIMINARY;		REMBLI	REMBL	REMBL	NE CO	(c)	AZOA;	EUTHERIA; ARTIODACTYLA.		N.A.	414.	UMI CO.	DA J.	6:869	EMBL; D70897; G1018989;		AA;	Query Match 30.1%;	rity	11; Conservative	ACS-N	-:	TCSCR
			T)	T)	E) 8	MBRA	(PI	KE	ARTI		ROM	7343	Ξı	TAKE	Sr.	97;		363		nila	.,	CRRK	<u>:</u>	CROK
			.199	-199.	-199	奥	ROFA	JTA;	(A)		国民	9	×		MON	2708	뎚.	띩	ď	ST	11	OEA		DOG!
-	002839	002839;	01-JUL-1997	-100-	-JAN-	RCINE	SUS SCROFA (PIG).	KARYC	THER	_	SEQUENCE FROM N.A.	MEDLINE; 97343414.	YOMUE	OUE ?	Į.	BL; I	MEMBRANE.	SEQUENCE	Matc	Loca	es	98 PI	=	2 PI
RESULT	8	8	0	0	5	М	Su	日日	B	二	SE	Ä	5 F	Z	I	邑	ME	SE	uery	est	Matches			
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EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA. [1] SEQUENCE FROM N.A. SIMS M.; SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS. LT 2
093473
093473
01-FEB-1997 (TREMBLREL. 02, CREATED)
01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
01-AN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
F14B4.1 (FRAGMENT).
CAENORHABDITIS ELEGANS.

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RESULT

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WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAM J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAM J., KIRSTEN J., LASTER N., LATREILLE P.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MISG J., THOMAS K., VAUDIN M., VAUGHAN K., WAITERSTON R.,
WAITSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
NATURE 368:32-38(1994).
                                                                                                                                                                                            EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY).
EUKRRYOTA: METAZOA; CHORDATA; VERTEBRATA: PISCES; GNATHOSTOMATA;
CHONDRICHTHYES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 70; DB 3; Length 426; Pred. No. 8.65e-01; 4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GATTUNG S., GCELA D., WILSON R.;
SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TREMBLREL. 04, LAST SEQUENCE UPDATE)
(TREMBLREL. 05, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RAVIN A.J., DYER S.M., YEADON J.E., BURDEN S.J.; J. PHYSIOL. (PARIS) 0:131-133(1991).
EMBL; M37645; G397971; -...
NON_TER PROSITE; PS01159; WW_DOMAIN_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 92064638.
YEADON J.E., LIN H., DYER S.M., BURDEN S.J.;
J. CELL BIOL. 115:1069-1076(1991).
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01, LAST SEQU
05, LAST ANNO
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                                                                                        CREATED)
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                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 27.3%;
Best Local Similarity 48.1%;
Matches 13; Conservative
                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                       01-JUL-1997 (TREMBLREL. 04,
                                                                                                                                       SIMILAR TO GALACTOKINASE
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01-NOV-1996 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
                                                                                                                                                                          ELEGANS
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                                                                                                                                                                                                                                           STRAIN-BRISTOL N2; MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE; 92064638.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                         CAENORHABDITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WATERSTON R.;
                                                                                                      01-JUL-1997
01-JAN-1998
                                                                                                                                                           M01D7.4.
                                    RESULT 9
ID 001969
AC 001969;
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Q91493
Q91493;
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PAITAN Y., BOULTON N., RON E., ROSENBERG E., ORR E.;
SUBMITTED (OCT-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!-CATALYITED (OCT-1917) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!-CATALYIC ACTIVITY: ATP-DEPENDENT BREAKAGE, PASSAGE AND REJOINING
OF DOUBLE-STRANDED DAY.
EMBL; AJ000543; E1168188; -.
FROSITE; PSOIJOIT7; TOPOISOMERASE_II; 1.
ISOMERASE; TOPOISOMERASE; ATP-BINDING.
SEQUENCE 815 AA; 89636 MW; 65A25520 CRC32;
                                                                                                                        Gaps
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MEDLINE; 92249159.
MEDLINE; 92249159.
RIGBY P.W.J.; CHAN C.T.J., TIMMONS P., ROBERTSON E.J., EVANS M.J., RIGBY P.W.J.; EVANS M.J., DEVELOPMENT 113:1105-1114(1991).
EMBL; X58196; G51133; -..
SEQUENCE 147 AA; 16309 MW; 6DC857F5 CRC32;
                                                                                                                                                                                                                                                                                                                                                          MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
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                                                                                   Score 73; DB 3; Length 1876; Pred. No. 2.65e-01; 5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28.1%; Score 72; DB 10; Length 147; Similarity 32.1%; Pred. No. 3.94e-01; 9; Conservative 9; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 72; DB 9; Length 815;
Pred. No. 3.94e-01;
2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; MYXOBACTERALES; MYXOCOCCACEAE.
                                                                                                                                                                                                                                                                                          CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                    DF107ECF CRC32;
                                                                                                                                                                                                                                                          147 AA
J. BIOL. CHEM. 271:13892-13899(1996).
EMBL: U52192; G1272420; --
FLYBASE: FBGNO015278; P13K6BD.
SEQUENCE 1876 AA; 210505 MW; DFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 CCNONHYTTCLRNLLQGEAERTDGVNIL 93
                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                       501 RRKTCT-RLYELISDQRTDDPELL 523
                                                                                                                                                                          691 PSCRRRSTWSCRLCAEHLRGAG 712
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01-JAN-1998 (TREMBLREL. 05,
01-JAN-1998 (TREMBLREL. 05,
                                                                                                                                                                                                                                                          PRELIMINARY;
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59.1%;
                                                                                   Query Match 28.5%;
Best Local Similarity 41.7%;
Matches 10; Conservative
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01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
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061639
061639;
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033367; JT 8 033367

RESULT

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Gaps

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Gaps
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SUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
SUTHERIA; ARTIODACIYLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 65; DB 4; Length 197; Pred. No. 5.80e+00; 2; Mismatches 3; Indels
                                                                                                                    Score 66; DB 9; Length 479;
Pred. No. 3.99e+00;
5; Mismatches 5; Indels
              KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL. D50458: 18105458; -
EMBL. 299106; E1182356; -
SEQUENCE 479 AA; 55166 MW; 3C2DIF5A CRC32;
                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
KRAPS. 5 KERATIN PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1
197 AA; 17474 MW; 731C19CA CRC32;
                                                                                                                                                                                                                                                                                               197 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JENKINS B.J., POWELL B.C.,
J. INVEST. DERMATOL. 103:310-317(1994).
EMBL. X73435; G313722; -.
                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                    Query Match
Best Local Similarity 41.2%;
Matches 7; Conservative
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Best Local Similarity 58.3%;
Matches 7; Conservative
                                                                                                                                                                                        207 RMYQLLKNAGKQVKTIM 223
                                                                                                                                                                                                             |:|:|| ||:: |:
15 RLYELLHGAGNHAAGIL 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
FISSUE-WOOL FOLLICLE;
MEDLINE; 94358466.
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SEQUENCE
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ID Q28584
AC Q28584;
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SSEERS
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Search completed: Thu Jul 30 09:09:09 1998 time: 21 secs.

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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu Jul 30 09:08:19 1998; MasPar time 3.18 Seconds 260.375 Million cell updates/sec Run on:

ular output not generated. Title:

>US-08-938-548A-3 (1-33) from USO8938548A.pep 256 1 QPLPDCCRQKTCSCRLYELLHGAGNHAAGILTL 33 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

69111 seqs, 25083644 residues Searched:

Post-processing: Minimum Match 08 Listing first 45 summaries

swiss-prot35 1:swiss1 Database:

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 31.693; Variance 44.992; scale 0.704

SUMMARIES

	Pred. No.	5.12e-02	1.20e-01	2.76e-01	4.17e-01	6.26e-01	6.26e-01	1.40e+00	1.40e+00	2.07e+00	2.07e+00	2.07e+00	2.07e+00	3.06e+00	3.06e+00	4.51e+00	4.51e+00	4.51e+00	4.51e+00	4.51e+00	4.51e+00	4.51e+00	6.60e+00	6.60e+00
	Description	CASPASE-11 PRECURSOR (PUTATIVE TRANSMEMBRANE	PUTATIVE ACID PHOSPHAT	60S RIBOSOMAL PROTEIN	SPERM MITOCHONDRIAL CA	PUTATIVE FORKHEAD-RELA	IG ALPHA CHAIN C REGIO	MEIOTIC RECOMBINATION	UDP-GLUCOSE 4-EPIMERAS	UDP-GLUCOSE 4-EPIMERAS	PHOSPHORIBOSYLAMINOIMI	INTERFERON-ACTIVATABLE	HYPOTHETICAL PROTEIN M	MITOCHONDRIAL INHERITA	OMEGA-AGATOXIN IIIA.	OMEGA-AGATOXIN IVB PRE	BOLA PROTEIN HOMOLOG.	AGOUTI SWITCH PROTEIN	AGOUTI SWITCH PROTEIN	AGOUTI SWITCH PROTEIN	VACUOLAR PROCESSING EN	PROTEIN ECSC.	ANGIOTENSINOGEN PRECUR
	Ω	ICEB_MOUSE	NMA_HUMAN	PPAW_CAEEL	R10A_TRYBR	MCS_MOUSE	YUL2_CAEEL	ALC_RABIT	RE11_SCHPO	GALE_RAT	GALE_HUMAN	PURK_PSEAE	IFIS_MOUSE	Y115_METJA	MD12_SCHPO	TXO3_AGEAP	TX4B_AGEAP	BOLA_HAEIN	AGSW_VULVU	AGSW_MOUSE	AGSW_HUMAN	VPE_VICSA	ECSC_BACSU	ANGT_MOUSE
	g :	н	Н	Н	н	н	Н	П	Н	7	н	Н	Н	н	н	Н	~	1	-1	-	 1	~1	-	1
	Length DB	373	260	450	214	197	461	299	923	347	348	360	425	155	273	9/	83	103	125	131	132	493	236	477
& Query	Match	29.3	28.5	27.7	27.3	27.0	27.0	26.2	26.2	25.8	25.8	25.8	25.8	25.4	25.4	25.0	25.0	25.0	25.0	25.0	25.0	25.0	24.6	24.6
	Score	. 75	73	71	70	69	69	67	67	99	99	99	99	65	65	9	64	64	64	64	64	64	63	63
Result	No.	7	7	m	4	S	Q	7	æ	6	10	11	12	13	14	12	16	17	18	19	50	21	22	23

29.3%; Score 75; DB 1; Length 373;

Query Match

6.60e+00	9.61e+00	9.61e+00	9.61e+00	9.61e+00	9.61e+00	1.39e+01	1.39e+01	1.39e+01	1.39e+01	1.39e+01	1.39e+01	1.39e+01	1.39e+01	2.01e+01	2.01e+01	2.01e+01	2.01e+01	2.01e+01	2.01e+01	2.01e+01	2.01e+01
TETRACYCLINE RESISTANC	UNC-6 PROTEIN PRECURSO	GLUTAMATE (NMDA) RECEP	GLUTAMATE (NMDA) RECEP	SPA2 PROTEIN.	MYOSIN HEAVY CHAIN, NO	GENE 34 PROTEIN.	UREASE OPERON URED PRO	UREASE OPERON URED PRO	HYPOTHETICAL PROTEIN K	TUBULIN BETA CHAIN.	PRPD PROTEIN.	GLYCINE BETAINE TRANSP	DNA REPAIR PROTEIN RAD	HYPOTHETICAL 37.9 KD P	MITOGEN-ACTIVATED PROT	HYPOTHETICAL 51.7 KD P	TETRACYCLINE RESISTANC	HYPOTHETICAL 118.6 KD	DNA POLYMERASE (EC 2.7	HYPOTHETICAL 133.0 KD	THYROGLOBULIN PRECURSO
TET9_ENTFA	UNC6_CAEEL	NME1_RAT	NME1_MOUSE	SPA2_YEAST	MY SO_HUMAN	VG34_HSVEB	URED_KLEAE	URED_KLEPN	Y129_HUMAN	TBB_TRYBR	PRPD_SALTY	BETP_CORGL	RAD5_YEAST	YHO5_YEAST	NTF6_TOBAC	YMT1_CAEEL	TETM_UREUR	YAF3 SCHPO	DPOL_ADE07	YIC6_YEAST	THYG BOVIN
П	Н	Н	н	Н	ч	٦	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	۲	Н
639	612	1464	1464	1466	1976	160	270	270	406	442	483	595	1169	334	371	471	639	1039	1122	1150	2769
24.6	24.2	24.2	24.2	24.2	24.2	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.4	23.4	23.4	23.4	23.4	23.4	23.4	23.4
63	62	62	62	62	62	61	61	61	61	61	61	61	61	9	09	9	9	9	9	9	9
24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Gaps

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THIS IMMUNOGLOBULIN BELONGS TO THE IGA-G SUBCLASS. IT WAS ISOLATED FROM A RABBIT HOMOZYGOUS FOR A2, N80, DE12,15, F71, G75 HEAVY
               NUCLEIC ACIDS RES. 12:1657-1670(1984).
-!- FUNCTION: IG ALPHA IS THE MAJON IMMUNOGLOBULIN CLASS IN BODY SECRETIONS. IT MAY SERVE BOTH TO DEFEND AGAINST LOCAL INFECTION AND TO PREVENT ACCESS OF FOREIGN ANTIGENS TO THE GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZESCHNIGK M., WILCKEN-BERGMANN B., STARZINSKI-POWITZ A.;
NUCLEIC ACIDS RES. 18:5289-5289(1990).
-!- FUNCTION: CATALYZES TWO DISTINCT BUT ANALOGOUS REACTIONS: THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1990 (REL. 16, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP-
 STOKLOSA C.M., SCHNEIDERMAN R.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 67; DB 1; Length 923; Pred. No. 1.40e+00;
                                                                                                                                                                                                                                                                                       Score 67; DB 1; Length 299;
Pred. No. 1.40e+00;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 923 AA; 107418 MW; B51C7725 CRC32;
                                                                                                                                                                                                                                                      594CED7C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
MEIOTIC RECOMBINATION PROTEIN REC11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           923 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 97231330.
LI Y.F., MUNATA M., WAHLS W.P., SMITH G.R.;
MCDL. MICROBIOL. 23:866-878(1997).
EMBL; U70737; G1619901; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       347 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     232 CCDIMRCLCLIVNKLSEKSNQTAEILVL 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                        299 AA; 32256 MW;
                                                                                                                                                                                   HSSP; P01857; 1PFC.
PROSITE; PS00290; IG_MHC; 2.
IMMUNOGLOBULIN C REGION.
                                                                                                                                                                                                                                                                                       26.2%;
llarity 50.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.2%;
Local Similarity 35.7%;
Les 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                 CHAIN HAPLOTYPE.
EMBL; X00353; G1576; -.
PIR; A02174; AHRB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SECTENCE FROM N.A.
TISSUE-SKELETAL MUSCLE;
MEDLINE; 90384840.
                                                                                  IMMUNOLOGIC SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RATIUS NORVEGICUS (RAI)
                                                                                                                                                                                                                                                                                                                                                         21
                                                                                                                                                                                                                                                                                                                                                                             1:|||| ::| :|
2 PLPDCCRQKTC-SC 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GALACTOSE 4-EPIMERASE)
                                                                                                                                                                                                                                                                                                                                                         44 PFPDCCPANSCCTC
                                                                                                                                                                                                                                                                                                       Local Similarity
les 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997
01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                           RE11_SCHPO
Q92380;
                                                                                                                                                                                                                                      NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LT 9
GALE_RAT
                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEIOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P18645;
                                                                                                                                                                                                                                                                                                          Best Loca
Matches
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ID GA
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                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAENORHABDITIS ELEGANS.
EUKARYOTA: METAZOA; ACOELOMATES; NEWATODA; SECERNENTEA; RHABDITIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
1G ALPHA CHAIN C REGION (FRAGMENT).
ORYCTOLAGUS CUNICULUS (RABBIT).
EUKARYOTA, METAZOA: CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                - DEVELOPMENTAL STAGE: LATE MEIOTIC AND EARLY HAPLOID CELLS
                 SUBCELLULAR LOCATION: KERATINOUS MITOCHONDRIAL CAPSULE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 69; DB 1; Length 461;
Pred. No. 6.26e-01;
6; Mismatches 5; Indels
                                                                                                                                                                                                                                                      Length 197;
                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                    MITOCHONDRION; SELENIUM; SPERM; TESTIS; SPERMATOGENESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PUTATIVE FORKHEAD-RELATED TRANSCRIPTION FACTOR F26A1.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBMITTED (JUN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-1- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
-1- SIMILARITY: CONTAINS A FORK-HEAD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WORMPEP; F26A1.2; CE02683.
PROSITE; PS00657; FORK_HEAD_1; 1.
PROSITE; PS00658; FORK_HEAD_2; 1.
PROSITE; PS50099; FORK_HEAD_3; 1.
HYPOTHET; DS50091; DNA-BINDING; NUCLEAR PROTEIN; TRANSCRIPTION REGULATION.
                                                                                                                                                                                                                                                    Score 69; UD 1,
Pred. No. 6.26e-01;
                                                                                                                                                                                   SELENIUM.
SELENIUM.
; 4E56990C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   262 FORK-HEAD.
54171 MW; FB2C37B7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                          461 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          299 AA
STRUCTURE OF THE SPERM MITOCHONDRIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                     34 S
21015 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27.0%;
Llarity 35.3%;
Conservative
                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 71.4",
10; Conservative
                                                                                                                                                                                                                                                      27.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     221 RHVLCKCQLFDVLQVEG 237
                                                                EMBL; M88463; G459886; -. EMBL; M29603; G567228; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 ROKTCSCRLYELLHGAG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                        123 PLKPPCCPQK-CSC 135
                                                                                                                                                                                                                                                                                                                                           2 PL-PDCCRQKTCSC 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U27312; G860690;
                                                                                                 PIR; A37199; A37199
HSSP; P01058; 1TAB.
                                                                                                                                 MGD; MGI:96945; MCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   461 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 6; Conser
                                                                                                                                                                                                                     197 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE; 84144059.
                                                                                                                                                                                                                                                                                                                                                                                                          T 6
YUL2_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FULTON L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALC_RABIT
P01879;
                                                                                                                                                                  BINDING
BINDING
BINDING
SEQUENCE
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SEQUENCE
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SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCAYNE J.D.,
KERLAVAGE A.R., DOUGHERY B.A., TOMB J.-F., ADAMS M.D., REICH C.I.,
OVERBEER R., KIRKNESS B.F., WEINSTOCK K.G., MERRICK J.M., GLODER A.,
SCOTT J.L., GEOGHAGEN N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D.,
UTTERBACK T.R., KELLEY J.M., PETERSON J.D., SADOW P.W., HANNA M.C.,
COTTON M.D., ROBERTS K.M., HORST M.A., KAINE B.P., BORDONSKY M.,
SCIENCE 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                              ARCHAEBACTERIA; EURYARCHAEOTA; METHANOCOCCALES; METHANOCOCCACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 65; DB 1; Length 155;
Pred. No. 3.06e+00;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 65; DB 1; Length 273;
Pred. No. 3.06e+00;
6; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BERGER K.H., SOGO L.F., YAFFE M.P.;
SUBMITIED (NOV-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-- SIMILARITY: TO YEAST MDM12.
EMBL, UG4674; G1655884;
MITOCHONDRION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SULT 15

1 TX03_AGEAP STANDARL,

2 P33034;

1 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)

1 01-OCT-1994 (REL. 28, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MDM12.
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL PROTEIN.
SEOUENCE 155 Aa; 17727 MW; 9D9D61E8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    273 AA; 30517 MW; 9024B3CC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M012_SCHPO STANDARD; PRT; 273 AA. 092377; CEL. 35, CREATED) 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE) 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE) MITOCHONDRIAL INHERITANCE COMPONENT MDM12.
                                                                                      01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
HYPOTHETICAL PROTEIN MJ0115.
                                        155 AA
                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 25.4%;
Best Local Similarity 53.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 25.4%;
Best Local Similarity 53.3%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                METHANOCOCCUS JANNASCHII
                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 CCR-OKTCSCRLYEL 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72 CCKITKPCPYRDYEL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           213 LLHGTGEHASSVI 225
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19 LLHGAGNHAAGIL 31
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                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A MEDLINE; 96337999
                    Y115_METJA
Q57579;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
RESULT ID MD AC 099 DT 011 DDT 011 DDT 011 DDT 011 DDT 011 DDT 011 DDE MI MDE M
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                                            Gaps
AGELENOPSIS APERTA (FUNNEL-WEB SPIDER).
EUKARYOTA; METAZOA; ARTHROPODA; CHELICERATA; ARACHNIDA; ARANEAE.
                                                                                                                                         ñ
                                                                                                                                         5; Indels
                                                                                                                         Length 76;
                                                                                                                          Score 64; DB 1; L
Pred. No. 4.51e+00;
                                                                                                                                         6; Mismatches
                                                                                                                                                        17 QCCRRNGYCSCYSLFGYLKSG 37
                                                                                                                                                                       5 DCCROKT-CSC-RLYELLHGA 23
                                                                                                                         Query Match
Best Local Similarity 38.1%;
Matches 8; Conservative
                             TISSUE=VENOM;
MEDLINE; 92129351
                       SEQUENCE
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Search completed: Thu Jul 30 09:08:29 1998 Job time : 10 secs.

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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu Jul 30 09:07:26 1998; MasPar time 4.27 Seconds 282.006 Million cell updates/sec ular output not generated. Run on:

>US-08-938-548A-3 (1-33) from US08938548A.pep 256 Description: Perfect Score: Title:

Scoring table:

Sequence:

1 QPLPDCCRQKTCSCRLYELLHGAGNHAAGILTL 33

PAM 150 Gap 11

120441 seqs, 36531193 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

1:pirl 2:pir2 3:pir3 4:pir4 5:nrl3d p1r56 Database:

Mean 30.310; Variance 51.743; scale 0.586 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		_	_	_	_	_	_	_	_	_	_	_	_	_	_	_	_	_	_	_	_	_	_	_
	Pred. No.	9.01e-01	1.84e+0(2.63e+0(2.63e+0(3.73e+0(5.28e+0(5.28e+0(7.44e+0(7.44e+00	7.44e+0(1.05e+01	1.05e+01	1.05e+01	1.46e+0]	1.46e+0]	1.46e+0]	1.46e+0]	1.46e+01	1.46e+0	1.46e+0]	1.46e+0]	1.46e+01	1.46e+01
	Description	hypothetical protein	dystrophin homolog -	oct2 protein isoform	sperm mitochondrial c	tetracycline-minocycl	Ig alpha chain C regi		Pglucose 4-epin	gene D3 protein - mou	transcriptional regul	hypothetical protein	keratin KAP5.5 - shee	beta-fructofuranosida	Omega-aga-ivb (nmr, m	Omega-aga-ivb (nmr, 2	omega-agatoxin-ivb -	omega-agatoxin IVB -	omega-agatoxin III, 8	omega-agatoxin IIIA -	omega-agatoxin III, 8	cell division protein	pigment deposition co	agouti protein precur
	А	524303	A41130	S60079	A37199	JN0800	AHRB	S09276	S11223	156329	B69764	C64314	146413	S33920	10MB	IOMA	1AGG	A44664	B54252	A42335	A54252	B64052	A46298	137143
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	Length DB	147	870	93	143	641	299	338	347	425	479	155	197	589	32	48	48	48	92	92	16	103	131	132
dР	Query	28.1	27.3	27.0	27.0	26.6	26.2	26.2	25.8	25.8	25.8	25.4	25.4	25.4	25.0	25.0	25.0	25.0	25.0	25.0	25.0	25.0	25.0	25.0
	Score	72	70	69	69	99	67	67	99	99	99	65	65	65	64	64	64	64	64	64	64	64	64	64
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44 E E E E E E E E E E E E E E E E E E	61
420202020202020202020202020202020202020	44

ALIGNMENTS

		hypothetical protein H19-3' - mouse	ISM #formal_name Mus musculus #common_name house mouse	13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change	10-Sep-1997	Ś	ENCE S24302	#authors Poirier, F.; Chan, C.T.J.; Timmons, P.M.; Robertson, E.J.;	Evans, M.J.; Riqby, P.W.J.	#journal Development (1991) 113:1105-1114		differentiation in vitro and at the time of implantation in	the developing embryo.	#accession S24303	##status preliminary	##molecule_type_mRNA	##residues 1-147 ##label POI	##cross-references EMBL:X58196; NID:q51131; PID:q51133	RY #length 147 #molecular-weight 16309 #checksum 6958	Query Match 28.1%; Score 72; DB 2; Length 147;	al Similarity 32.1%; Pred. No. 9.01e-01;	ches 9; Conservative 9; Mismatches 10; Indels 0; Gaps 0;	66 CCNQNHYTTCLRNLLQGEAERIDGVNIL 93
RESOLL	ENTRY	TITLE	ORGANISM	DATE		ACCESSIONS	REFERENCE	#autho		#jourr	#title			#acces	3##	44	C##	**	SUMMARY	Query 1	Best K	Matches	99 qa

6 CCRQKTCSCRLYELLHGAGNHAAGILTL 33 ò

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A41130 #type fragment dystrophin homolog - Pacific electric ray (fragment) 3300k subsynaptic protein #formal_name Torpedo californica #common_name Pacific ALTERNATE_NAMES ORGANISM ACCESSIONS REFERENCE RESULT ENTRY DATE

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#superfamily immunoglobulin C region; immunoglobulin homology
immunoglobulin
                                                 #superfamily immunoglobulin C region; immunoglobulin homology
duplication; glycoprotein; heterotetramer; immunoglobulin;
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#title cDNA from rat cells with reconstitutive galactose-epimerase activity in E. coli.
#cross-references MUID:90384840
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stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.
                                                                                                            #domain immunoglobulin homology #label IGG1\
#domain immunoglobulin homology #label IGG2\
#binding_site carbohydrate (Asn) (covalent) #status
predicted
                                                                                                                                                                                                                                                                                                                                                                              $69276  #type fragment
Ig alpha chain c region - rabbit (fragment)
#formal_name Oryctolagus cuniculus #common_name domestic
rabbit
                                                                                                                                                                                                                                                            Gaps
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UDPgalactose 4-epimerase
#formal_name Rattus norvegicus #common_name Norway rat
18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change
08-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #authors Burnett, R.C.; Hanly, W.C.; Zhai, S.K.; Knight, K.L. #journal EMBO J. (1989) 8:4041-4047
#title The 194 heavy-chain gene family in rabbit: cloning and sequence analysis of 13 C-alpha genes.
#cross-references Mul
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larity 50.0%; Pred. No. 5.28e+00;
Conservative 4; Mismatches 2; Indels
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Pred. No. 5.28e+00;
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Best Local Similarity 50.0%;
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S09276
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2 PLPDCCRQKTC-SC 14
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2 PLPDCCRQKTC-SC 14
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##residues 1-3
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Matches 7; Conserv
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#authors
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Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.;
Bolotin, A.; Borchert, S.; Boriss, R.; Boursier, L.; Brans,
A.; Braun, M.; Bridwell, S.C.; Bron, S.; Broulllet, S.;
Bruschi, C.V.; Caidwell, B.; Capuano, V.; Carter, N.M.;
Choi, S.K.; Codani, J.J.; Connerton, I.F.; Cummings, N.J.;
Barleh, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J.;
Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fujita,
M.; Fujita, Y.; Funa, S.; Galizzi, A.; Galleron, N.; Ghim,
S.Y.; Glaser, P.; Goffeau, A.; Golightly, E.J.; Grandi, G.;
Guiseppi, G.; Guy, B.J.; Haga, K.; Halech, J.; Harwood,
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#formal_name Mus sp. #common_name mouse
26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
28-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tannenbaum, C.S.; Major, J.; Ohmori, Y.; Hamilton, T.A. J. Leukoc. Biol. (1993) 53:563-558
A lippolysaccharide-inducible macrophage gene (D3) is a member of a literferon-inducible gene cluster and is selectively expressed in mononuclear phagocytes.
                                                                                                                                                                                                                                                                                                                                               Gaps
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05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
05-Dec-1997
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transcriptional regulator (GntR family) / homolog ycnF
Bacillus subtilis
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                                                                                                    #superfamily Escherichia coli UDPglucose 4-epimerase; UDPglucose 4-epimerase homology
                                                                                                                                                                                                             #domain UDPglucose 4-epimerase homology #label 6
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#length 425 #molecular-weight 47046 #checksum
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Pred. No. 7.44e+00;
10; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                         2; Indels
##residues 1-347 ##label ZES
##cross-references EMBL:X53949; NID:957791; PID:957792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##residues 1.425 ##label RES ##cross-references GB:S62227; NID:9385702; PID:9385703
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Pred. No. 7.44e+00;
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#accession I56329
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Best Local Similarity 31.0%;
Matches 9; Conservative
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A69580
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#submission submitted to the Brookhaven Protein Data Bank, September 1993
#cross-references PDB:10MA
COMMENT Resolution: not applicable
COMMENT Determination: NAR
#domain signal sequence #status experimental #label SIG\
#product beta-fructofuranosidase #status experimental
#label MAT\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #authors Yu, H.; Rosen, M.K.; Schreiber, S.L.
#submission submitted to the Brookhaven Protein Data Bank, September 1993
#cross-references PDB:10MB
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                                                                                #binding_site carbohydrate (Asn) (covalent) #status
predicted\
#binding_site phosphate (Thr) (covalent) #status
predicted\
#binding_site phosphate (Ser) (covalent) #status
predicted
#length 589 #molecular-weight 63650 #checksum 1032
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funnel-weaving spider (Agelenopsis aperta)
#formal_name Agelenopsis aperta
A51323
                                                                                                                                                                                                                    Length 589,
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Pred. No. 1.05e+01;
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Pred. No. 1.46e+0
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#region turn (type II)\
#disulfide_bonds\
#disulfide_bonds\
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#length 35 #molecula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #disulfide_bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Resolution: not applicable Determination: NAR
                                                                                                                                                                                                                                                                                  548 RLFDVLNG-GEQAIETLDL 565
                                                                                                                                                                                                                                                                                                      Query Match 25.4%;
Best Local Similarity 42.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 45.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 25.0%;
Best Local Similarity 45.5%;
Matches 5; Conservative
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13-16
4-20
12-25
19-36
27-34
                                                36,42,170,188,211,
254,259,318,322,
388,463,518,527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7-9,31-33,23-24
10-13
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                                                                                                                                                   458,475,490
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 1-23
24-589
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REFERENCE
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24-31
SUMMARY
                                                                                                                  70,92
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                                                                                                                                                                                    SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                     ENTRY
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Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Db 19 CCRGRPCRCSM 29

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Qy 6 CCRQMTCSCRL 16

Search completed: Thu Jul 30 09:08:01 1998
Job time: 35 secs.
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu Jul 30 09:09:28 1998; MasPar time 1.19 Seconds 161.980 Million cell updates/sec ular output not generated. :uo

>US-08-938-548A-3 (1-33) from US08938548A.pep 256 1 QPLPDCCRQKTCSCRLYELLHGAGNHAAGILTL 33

Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

Minimum Match 0% Listing first 45 summaries Post-processing:

63816 seqs, 5850866 residues

Searched:

Database:

Statistics:

Mean 21.451; Variance 82.349; scale 0.260 a-issued 1:5_COMB 2:PCT9_COMB 3:backfiles

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

*				
Query Match Length DB		ΩI	Description	Pred. No.
25.8 39 1		US-08-249-	Sequence 40, Applicati	2.23e+01
39		US-08-036-	40,	2.23e+01
25.8 39 2		PCT-US95-0	40,	2.23e+01
25.8 39 2		PCT-US94-0	40,	2.23e+01
25.8 39 1		us-08-469-	40,	2.23e+01
		PCT-US95-0	2, A	2.23e+01
25.0 1167 1		US-08-485-	ý	3.29e+01
٥.		US-08-620-	6	3.29e+01
4.2		DS-08-056-	1,	4.83e+01
23.8 42 1		US-08-487-	23,	5.85e+01
m		US-08-480-	23,	5.85e+01
m		US-08-477-	23,	5.85e+01
23.8 42 1		US-08-137-	23,	5.85e+01
23.8 59 1		US-08-233-	Sequence 51, Applicati	5.85e+01
23.4 222 3		5223425-6	52	7.08e+01
		US-08-279-	Sequence 10, Applicati	7.08e+01
		us-08-658-	Sequence 2, Applicatio	8.55e+01
23.0 1019 1		ns-08-296-	4,	8.55e+01
23.0 1083 1		us-08-296-	'n	8.55e+01
22.3 21 1		US-08-019-	ď,	1.24e+02
m.		US-08-379-	1	1.24e+02
22.3 724 1		US-08-121-	62,	1.24e+02
22.3 724 2	_	PCT-US94-1	62,	1.24e+02

11.224	ni, Mark;	
te 2, Application 20, Application 20, Application 20, Application 3, Application 3, Application 20, 217308. No. 517308. No. 517308. No. 5475086. No. 5475086. 1 Application 2, Application 2, Application 3, Application 3, Application 3, Application 2, Application 3, Applic	Paul; Michael; Marchioni,	kb storage
Sequence 20 Sequence 20 Sequence 20 Sequence 30 Sequence 30 Sequence 40 Sequence 40 Patent No. Patent No. Patent No. Sequence 11 Sequence 12 Sequence 20 Sequence	obant, rifeld, rifeld, lc Factor of Use	inch, 360 k 9,322A 55 73 89
US-08-363- US-08-446- US-08-446- US-08-357- US-08-08-09-1 US-08-09-1 US-08-117-	IGNME 082493 082493 1183; 1181; 1111 in Mit aratilaratutue	3/24 3/24 35,1 55,1 10,3
	STAN on U ion rl, ftti, ftti, ftti, fit fi sississississississississississississi	COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 5. COMPUTER: IBM OPERATING SYSTEM: PC-DOS SOFTWARE: Wordperfect CURRENT APPLICATION DATA: APPLICATION NUMBER: US/06 FILING DATE: 26 MAY-1994 CIALING DATE: 24 MAR-1993 FILING DATE: 24 WAR-1993 FILING DATE: 23 CT-1992 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/96 FILING DATE: 23 CCT-1992 PRIOR APPLICATION NUMBER: 07/96 FILING DATE: 03 SEP-1992 PRIOR APPLICATION NUMBER: 07/96 FILING DATE: 30 JUN-1992 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/96 FILING DATE: 30 JUN-1992 PRIOR APPLICATION DATA:
23 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	322A-40 STAND 0, Application US 1, 5716910 1. 5716910 1. 17169210 1. 17169210 1. 17169210 1. 17169210 1. 1717 1. 1717 1. 1717 1. 1717 1. 1717 1. 1022 1. 1022 1. 1022 1. 1717 1. 1022	COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM OPERATING SYSTEM: PC-: SOFTWARE: Wordperfect CURRENT APPLICATION DATA APPLICATION NUMBER: U FILING DATE: 26-MA'-1 CLASSIFICATION: 435 APPLICATION WEBER: 0 FILING DATE: 24-MA'-1 APPLICATION NUMBER: 0 FILING DATE: 23-CCT-1 RIOR APPLICATION DATA: APPLICATION NUMBER: 0 FILING DATE: 03-SEP-1 RIOR APPLICATION DATA: APPLICATION NUMBER: 0 FILING DATE: 03-SEP-1 RIOR APPLICATION DATA: APPLICATION NUMBER: 0 FILING DATE: 33-CCT-1 RIOR APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATE: 30-JUN-1 RIUNG DATE: 30-JUN-1
	9-322 40, 00-50, 00-10, 10ANT	COMPUTER READA MEDIUM TYPE: COMPUTER: OMENATING SY SOFTWARE: WISSETTING SY SOFTWARE: WISSETTING DATE: PRIOR APPLICATION PRIOR APPLICATION FILING DATE: PRIOR APPLICAT
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40000000000000000000000000000000000000	SOL	888888888888888888888888888888888888888

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TYPE: amino acid STRANDEDNESS:
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AC XXXXXX
AC XXXXXX
DY XX SEQUENCE 40, APPLICAX
C SEQUENCE 1 INVERNATION OF TITLE OF INVENTY
CC APPLICAXT: GLOST OF TITLE OF INVENTY
CC APPLICAXT: GLOST OF TITLE OF INVENTY
CC APPLICAXT: GLOST OF TITLE OF INVENTY
CC CONTRESPONDENCE APPLICATION OF TITLE OF TI
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                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
             8888888888888888
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GENERAL INFORMATION:
APPLICANT: Robert Sklar, Mark Marchionni,
APPLICANT: David I. Gwynne
TITLE OF INVENTION: MCSCLE CONDITION
NUMBER OF SEQUENCES: 185
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
ZIP: 02110-2804
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360
MEDIUM TYPE: kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 66; DB 2; Lv
Pred. No. 2.23e+01;
FILING DATE: 03-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 30-JUN-1992
PRIOR APPLICATION NUMBER: 07/863,703
FILING DATE: 03-APRIL-1992
PRIOR APPLICATION NUMBER: 07/863,703
FILING DATE: 03-APRIL-1991
APPLICATION NUMBER: 0.K, 91 07566.3
FILING DATE: 10-APRIL-1991
ATTORNEY/AGENT INFORMATION:
NAME: HANSON, NOTMAN D.
REGISTRATION NUMBER: 130,946
REFERENCE/DOCKET NUMBER: LUD 5250.5
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 838-384
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OCHEVIER: 150
CORTULER: 150
CORTULER: 150
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05083C
FILING DATE: 06-MAY-94
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,204
FILING DATE: 08-MAR-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/059,022
FILING DATE: 06-MAY-93
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
CE 39 AA; 3760 MW; 6521 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 25.8%;
Best Local Similarity 70.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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Sequence 40, Application US/08469569
Patent No. 5606032
GENERAL INFORMATION:
APPLICANT: Goodearl, Andrew; Stroobant, Paul;
APPLICANT: Chen, Maio Su; Hiles, Ian
TITLE OF INVENTION: Preparation and Use
NUMBER OF SEQUENCES: 184
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREE: New York City
CITY: New York City
                                                                                                                                                                                                                                                                                                                                                                                                                              ï
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39 AA.
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 04585/028WO1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPHONE: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                           Score 66; DB 2; L
Pred. No. 2.23e+01;
1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOCTHWARE: Wordberfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,569
FILING DATE: 06-UNV-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/036,555
FILING DATE: 24-MAR-1993
APPLICATION NUMBER: 07/865,173
FILING DATE: 23-OCT-1992
RIOR APPLICATION DATA:
APPLICATION NUMBER: 07/865,173
FILING DATE: 03-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/940,389
FILING DATE: 03-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/907,138
FILING DATE: 30-UNW-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/863,703
FILING DATE: 03-APRIL-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/863,703
FILING DATE: 03-APRIL-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 40, Application US/08469569
                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
ICE 39 AA; 3760 MW; 6521 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                           Query Match 25.8%;
Best Local Similarity 70.0%;
Matches 7; Conservative
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Sequence 1, Application US/08026138E
Patent No. 5502166
GENERAL INFORMATION:
APPLICANT: MASAYOSH! MISHINA
TITLE OF INVENTION: NOVEL PROTEINS AND GENES CODING THE SAME
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nishtohata-mach!
CITY: Nilgata-sh!
STREET: 5214, Nishiohata-mach!
CITY: Nilgata-sh!
STATE: Nilgata-sh!
STATE: Nilgata-sh!
STATE: DAPAN
ZIP: 951
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
                                                                                                                       Gaps
                                                                                                                     ö
                                                                         Length 1168;
                                                                                                                       3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE TYPE: Cerebellum
PUBLICATION INFORMATION:
AUTHORS: Masayoshi MISHINA
TITLE: NOVEL PROTEINS AND GENES CODING THE SAME
                                                                                                                                                                                                                                                                                                                 1464 AA
                                                                      Score 64; DB 1; Le
Pred. No. 3.29e+01;
3; Mismatches 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/026,138E
FILING DATE: 26-FEB1993
PRIOR APPLICATION NUMBER: US/08/026,138E
FILING DATE: 26-FEB1992
APPLICATION NUMBER: UP 13155/1992
FILING DATE: 30-JUN-1992
APPLICATION NUMBER: UP 173155/1992
FILING DATE: 12-AUG-1992
APPLICATION NUMBER: UP 303878/1992
FILING DATE: 13-NOV-1992
APPLICATION NUMBER: UP 303878/1992
FILING DATE: 13-NOV-1992
APPLICATION NUMBER: UP 303878/1992
FILING DATE: 13-NOV-1992
APPLICATION NUMBER: 22,389
REFERENCE/OCKET NUMBER: 22,389
REFERENCE/OCKET NUMBER: F-4551
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 953-7733
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
  INDIVIDUAL ISOLATE: 167p
SEQUENCE 1168 AA; 131542 MW; 7175894 CN;
                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08026138E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYSTEM: MS-DOS v.5
Word Perfect 5.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1464 amino acids
TYPE: amino acid
STRANDEDNESS: single stra
                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                    Query Match
Best Local Similarity 45.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
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                                                                                                                                                                                                                 4 PDCCROKICSC 14
                                                                                                                                                                                                                                                                                 RESULT 9

ON CONTRACT NO. 550216

CC GENERAL INFORMAT

CC COUNTRY: Main

CC COUNTRY: JA.

CC CONTRESPONDENCE

APPLICATION FOR

CC CONTRESPONDENCE

CONTRESPON
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Patent No. 5670365
GENERAL INFORMATION:
APPLICANT: Feitelson, Jerald S.
TITLE OF INVENTION: Identification of, and Uses For, Nematicidal
TITLE OF INVENTION: Bacillus thuringlensis Genes, Toxins, and Isolates
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                            Score 64; DB 1; Length 1167;
Pred. No. 3.29e+01;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1168 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1 CITY: Gainesville STATE: Florida COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: MA48DD2.C1 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                       MOLECULE TYPE: protein
FENCE 1167 AA; 131657 MW; 7095219 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUFTWARE: PATENTIANS SUFTWARE: CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/620,717A
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBB PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/08620717A
                                       TELEPHONE: (904) 375-8100
TELEPAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 1167 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1168 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 45.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
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4 PDCCRQKTCSC 14
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US-08-620-717A-9
                                                                                                                                                                                                                                                                  SEQUENCE
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RESULT

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APPLICANT: Cruz, Lourdes J.
APPLICANT: Cruz, Lourdes J.
APPLICANT: McIntosh, J. Michael
APPLICANT: McIntosh, J. Michael
APPLICANT: Santos, Ameurfina D.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Indels
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Pred. No. 5.85e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,800
FILING DATE: 19-CCT-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-10476
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
                                                                                                                                                                                                                                                                                                                          CITY: Washington
STATE: DC
21P: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                        Sequence 23, Application US/08137800 Patent No. 5514774 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 51, Application US/08233788A
                                                                              Sequence 23, Application US/08137800
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42 AA; 4618 MW; 9505 CN;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide HYPOTHETICAL: NO
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Best Local Similarity 47.4%;
Matches 9; Conservative
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ORGANISM: COI
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AC XXXXXX
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DD Sequence 51, Applic
XX
C Sequence 51, Applic
C Patent No. 5635617
CC GENERAL INFORMATI
CC APPLICANT: DOR
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                                                                                                                                                                                                                         APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hallyard, David R.
APPLICANT: Macintosh, J. Michael
APPLICANT: Santos, Ameurfino S.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.

ZIP: 2005

ZIP: 2005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATIOS SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,383

FILING DATE: 10-071-1995

REPLICATION NUMBER: US 08/137,800

FILING DATE: 19-071-1993

PRIOR APPLICATION NUMBER: US 08/084,848

FILING DATE: 29-010-1993

ATORNEY/AGENT INFORMATION:

NAME: Ihnen, Jeffrey L.

REGISTRATION NUMBER: 28,957

REFERENCE/DOCKET NUMBER: 24,260-107673

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
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                                              42 AA
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Pred. No. 5.85e+01;
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                                              PRT;
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                                                                                                                                                                            Sequence 23, Application US/08477383 Patent No. 5589340 GENERAL INFORMATION:
                                                                                                                                             Sequence 23, Application US/08477383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL: NO CORIGINAL SOURCE: ORGANISM: Conus ochroleucus JENCE 42 A8; 4618 MW; 9505 CN;
                                              STANDARD;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGIH: 42 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 23.8%;
Best Local Similarity 47.4%;
Matches 9; Conservative
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                                          US-08-477-383-23
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US-08-137-800-23
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Gaps

SEQUENCE

RESULT ID US-

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

on: Thu Jul 30 09:06:53 1998; MasPar time 3.32 Seconds 152.287 Million cell updates/secular output not generated.

Title: >US-08-938-548A-3
Description: (1-33) from US08938548A.pep
Perfect Score: 2-6
Sequence: 1 QPLPDCCRQKTCSCRLYELLHGAGNHAAGILTL 33

Scoring table: PAM 150 Gap 11 Searched: 124785 seqs, 15338987 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq31-2 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27

Statistics: Mean 22.991; Variance 84.736; scale 0.271

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ					
Result No.	Score	Query	Length DB	DB	Ð	Description	Pred. No.
-	77	30.1	363	33	W12414	Porcine complement in	6.25e+00
7	75	29.3	373	18	R98461	Murine ICE-ced-3 homo	9.46e+00
Ė	75	29.3	373	13	R66767	Murine interleukin-1	9.46e+00
4	69	27.0	329	5 6	W29877	Lysophosphatidic acid	3.20e+01
5	99	25.8	102	٦	P95679	Xenopus Vq1 protein f	5.80e+01
9	99	25.8	348	20	W01619	Human uridine diphosp	5.80e+01
7	65	25.4	78	'n	P20020	Sequence of a foot an	7.06e+01
80	64	25.0	45	53	W10106	Human agouti signalli	8.59e+01
σ	64	25.0	45	23	W10105	Murine agouti signall	8.59e+01
10	64	25.0	48	σ	R45611	AG1 toxin.	8.59e+01
11	64	25.0	48	Ξ	R60293	Calcium channel inhib	8.59e+01
12	64	25.0	48	ω	R44209	A. aperta venom fract	8.59e+01
13	64	25.0	130	23	W10102	Human agouti signalli	8.59e+01
14	64	25.0	131	23	W10101	Murine agouti signall	8.59e+01
15	64	25.0	1167	27	W31504	Nematode toxin 167P p	8.59e+01
16	64	25.0	1167	2	W10653	Bacillus thuringiensi	8.59e+01
17	64	25.0	1168	23	W16326	Nematocidal toxin 167	8.59e+01
18	62	24.2	34	10	R55088	Tarantula spider veno	1.27e+02
19	62	24.2	1464	10	R55529	Human NMDA R2A recept	1.27e+02

1.27e+02 1.27e+02 1.27e+02 1.27e+02 1.53e+02 1.53e+02 1.53e+02 1.53e+02 1.53e+02 1.53e+02 1.53e+02 1.86e+02 1.86e+02 1.86e+02 2.24e+02 2.24e+02 2.24e+02 2.24e+02	2.71e+02 2.71e+02 2.71e+02 2.71e+02 2.71e+02
Human N-methyl-D-aspa Human excitatory amin Glutamic acid recepto Rat NMDA receptor sub A-lineage conotoxin p Predatory cone snail Salmonella entritidi Human membrane antige TctA sequence. Human bg protein asso Gyn d allergen Bl. Cherry polyphenol oxi E. coli DNA polymerase DNA polymerase III ho APP-HCV-E2 fusion pro Spider venom peptide N-terminal sequence o Funnel-web spider ven Connexin-32.	Sequence of viber ven Sequence of viber ven Ovine FSH beta subuni Ikaros protein. Mouse 22B/30B (candid Murine Lystl long iso
R66039 R80970 R44192 W124492 W124490 W24890 W23579 W23579 W23571 W23671 R40105 R40115 R40115 R40115 R40115 R40115 R40115 R40115 R40115 R40115	P91095 R10038 R92020 W31948 W23594
118 118 118 122 122 123 133 148 168 178 178 188 178 178 178 178 178 178 17	37 27 25 25
14664 14664 14664 14664 14664 1460 1460	49 129 334 2186 3788
444446666666666666666666666666666666666	222. 222. 7.22. 7.22. 7.22. 7.22.
000000000000000000000000000000000000000	00000000000000000000000000000000000000
0.000000000000000000000000000000000000	64444 44444 2443

ALIGNMENTS

Query Match 30.1%; Score 77; DB 23; Length 363; Best Local Similarity 39.3%; Pred. No. 6.26e+00; Matches 11; Conservative 7; Mismatches 9; Indels 1; Gaps

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98 plqeacrrkacs-nlpdplngqvsypng 124 | | : || : | : | : | | | : | | 2 PLPDCCRQKTCSCRLYELLHGAGNHAAG 29

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RESULT 2
ID R98461 standard; Protein; 373 AA.
AC R98461,
DT 25-SEP-1996 (first entry)
DE Murine ICE-ced-3 homologue.
KW mICh-2; murine ICE-ced-3 homologue; programmed cell death;

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Sequence
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Matches
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ID W1
AC W1
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congenital craniofacial and other skeletal or dental anomalies, induction
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                    of local endochondral bone formation in non-union fractures, peridontal applens. requiring bone formation and cartilage repair, eg in the treatment of osteoarthitis:
See also P95679-P95692 and N95097.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human mature unidate diphosphate galactose-4-epimerase (UDP-G4E) (W01619) catalyses a reversible reaction between UDP-glucose and UDP-galactose that allows galactose residues to enter into the main pathways of glucose metabolism. A deficiency of the enzyme results in galactosaemia. The amino acid sequence of UDP-G4E was deduced from a cDNA clone (158301) derived from a human endometrial tumour library. Recombinant UDP-G4E polypeptides can be produced in transformed host (e.g. E. coli, COS, Sf9 insect) cells or expressed in vivo for use in the treatment of UDP-G4E deficiency, e.g.
                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding human uridine diphosphate galactose-4-epimerase - used in the treatment and diagnosis of galactosaemia Claim 1; Page 43-44; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Uridine diphosphate galactose-4-epimerase; UDP-G4E; galactosaemia;
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Pred. No. 5.80e+01;
4; Mismatches 2; Indels
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                                                                                                                                                        Length 102;
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                                                                                                                                                        DB 1; Le
                                                                                                                                                                                                   Mismatches
                                                                                                                                                        Score 66;
Pred. No.
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W01619 standard; Protein; 348 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-MAY-1995; U05785.
11-MAY-1995; WO-U05785.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25.8%;
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Similarity 56.3%;
9; Conservative
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                                                                                                                                                                                                                                                                     12 CSCRLYELLHGAGNHA 27
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GB-011064.
GB-025150.
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                                                                                                                                                        Query Match
Best Local Similarity
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sst_Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ji H, Rosen CA;
WPI; 96-518666/51.
N-PSDB; T58301.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           therapy; diagnosis
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WO9635778-A1.
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                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human agouti signalling protein fragment #2.
Agouti signalling protein; ASP; depigmenting activity; cosmetic;
Apperpigmentary condition; melasma photroageing spots; solar keratosis;
post-inflammatory hyperpigmentation; wound healing; eumelanogenesis;
vitiligo; leucoderma; albinism; hair greying.
                                                                                                                                                                                                DNA correspo. to (part of) foot and mouth disease virus RNA - useful in prepo. of vaccines for producing antibodies against the virus Example; Fig 6: 57pp: English.

The inventors claim a DNA molecule comprising a nucleotide sequence corresp. to all or a portion of foot-and-mouth disease virus RNA (FMMY). The DNA molecule is esp. for a precursor of FMDV engals or protein. It esp. codes for FMDV protein p88 and vPl-vP4. It may code for VP4, VP2 vP3 and vPl contiguously. The inventors also claim a vaccine for stiunlating prodn. of antibodies against FMDV in a mammal which comprises at least one of the above recombinant proteins produced by a host cell transformed with the DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hyperpigmentary conditions and diseases such as melasma photoageing spots, solar keratosis, and post-inflammatory hyperpigmentation such occurs at sites of wound healing. They can also be used to provide enhanced eumelanogenesis for treating eg. vitiligo, leucoderma, some
                                                                                                                                                                                             - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
(NATE ) National Res Dev Corp.

(WELL ) Wellcome Foundation Ltd.

Boothroyd JC. Cross GAM, Highfield PE, Winther MD, Rowlands DJ,

Brown F, Harris TJR, Lowe PA;

WPI; 82-26702E/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 65; DB 5; Length 78; Pred. No. 7.06e+01; 9; Mismatches 5; Indels
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21-JUN-1996; U10695.
23-JUN-1995; US-000436.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           forms of albinism and hair greying.
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W10105 standard; protein; 45 AA.
W10105;
17-SEP-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45 qntcsthtygglhst-thstlvls 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 OKTCSCRLYELLHGAGNHAAGILT 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jr 8
W10106 standard; protein; 45 AA.
W10106;
18-SEP-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25.0%;
41.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 37.5%;
Matches 9; Conservative
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WPI; 97-087323/08
                                                                                                                                                                           N-PSDB; N20019.
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9.0

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Pacillus thuringlensis toxin gene - useful in recombinant hosts, particularly plants for the control of nematodes Claim 4; Page 35-39, 44pp. English.

This sequence represents the protein encoded by a polynucleotide of the Invention. The polynucleotide of the Invention is a sequence from a Bacillus thuringlensis (Bt) isolate selected from PS80JJ1, PS158D5, PS167P, PS169B, PS177F1, PS177G, PS20464 and PS204G6, that encodes a toxin active against nematodes. This sequence represents the 167P protein, and is a delta-endotoxin protein. The polynucleotides and toxins can be used for the control of nematode pests such as Panagrellus
   Agouti signalling protein; ASP; depigmenting activity; cosmetic; hyperpigmentary condition; melasma photoageing spots; solar keratosis; post-inflammatory hyperpigmentation; wound healing; eumelanogenesis; vitiligo; leucoderma; albinism; hair greying.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New agouti signal protein peptide(s) and nucleic acids - used for altering melanin prodn., for treating e.g. melasma photo-ageing spots, solar keratosis or vitiligo claim 5; Page 8-9; 67pp; Engalish.

The sequences given in W10101-29 are biologically active peptides and fragments of the agouti signalling protein (ASP) which have depigmenting activity. These peptides are useful for cosmetic purposes and for clinical application in the prevention or treatment of various hyperpigmentary conditions and diseases such as melasma photoageing spots, solar keratosis, and post-inflammatory hyperpigmentation such as occurs at sites of wound healing. They can also be used to provide enhanced emmelanogenesis for treating eg. vitiligo, leucoderma, some
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Nematode toxin 167P protein.
PCR primer; amplify; nematode toxic protein; Bacillus thuringiensis; delta-endotoxin gene; nematode pest control; Panagrellus redivivus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 64; DB 23; Length 131;
                                                                                                                                                                                                                                                                                                                                                                     "Start of Cysteine-rich motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 8.59e+01;
                                                                                                                                                                                                                                                                                                     'note= "Start of basic region"
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                                                                                                                                                                                                        1..21
/note= "Signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     forms of albinism and hair greying.
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W31504 standard; Protein; 1167
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Matches 7; Conservative
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21-MAR-1996; U04755.
21-MAR-1996; US-590554.
(MYCO ) MYCOGEN CORP.
Fu J, NAIVA KE, PAYNE J; 97-480163/44.
N-PSDB; T89185.
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Bacillus thuringiensis.
WO9734926-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-000436
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21-JUN-1996; U10695.
23-JUN-1995; US-0004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 97-087323/08.
                                                                                                                                     Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                   WO9700892-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          claim 6; Page 8-9; 67pp; English.
The sequences given in W1010-29 are biologically active peptides and fragments of the agouti signalling protein (ASP) which have depigmenting activity. These peptides are useful for cosmetic purposes and for clinical application in the prevention or treatment of various hyperpigmentary conditions and diseases such as melasma photoageing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human agouti signalling protein.
Agouti signalling protein.
Agouti signalling protein; ASP; depigmenting activity; cosmetic;
hypersignentary condition; melasma photoageing spots; solar keratosis;
post-inflammatory hyperpigmentation; wound healing; eumelanogenesis;
vitiligo; leucoderma; albinism; hair greying.
Example; Page 17; 28pp; English.

The sequence is that of a polypeptide present in fraction K of the venom of Agelenopsis aperta, it blocks calcium channels in cells of both mammals and invertebrates, partic. those affecting neuronal and muscle cells. It may be used in the treatment of angina, hypertension, cardiomyopathies, supraventricular arrhythmia, oesophogeal achalasia, premature labour, and Raynaud's disease. It may also be of use in the study of cell physiology and in the control of invertebrate pests. It may be produced synthetically. Sequence 48 AA;
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New agout1 signal protein peptide(s) and nucleic acids - used for altering melanin prodn., for treating e.g. melasma photo-ageing spots, solar keratosis or vitiligo
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Pred. No. 8.59e+01;
3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                 Score 64; DB 8; Length 48;
Pred. No. 8.59e+01;
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86
                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Signal sequence"
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Sequence 130 AA;
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W10102 standard; protein; 130 AA
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Best Local Similarity 41.28;
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21-JUN-1996; U10695.
23-JUN-1995; US-000436.
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Best Local Similarity
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu Jul 30 09:04:06 1998; MasPar time 9.31 Seconds 592.652 Million cell updates/sec lar output not generated. on O

>US-08-938-548A-2 (1-131) from US08938548A.pep 931 Description: Perfect Score: Sequence: Title:

1 MNLPSTKVSWAAVTLLLLLLL......GRRCSAPAAASVAPGGQSGI 131

PAM 150 Gap 11 Scoring table:

140542 seqs, 42109429 residues

Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

sptrembl5
1:sp_fung1 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_macteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Mean 39.725; Variance 90.808; scale 0.437 Statistics:

SUMMARIES

i i	Wo.	Score	* Query Match	* Query Match Length DB	DB	£	Description	Pred. No.
i	П	109	11.7	602	2	962731	PROSTAGLANDIN H SYNTHA	2.09e-02
	7	108	11.6	599	7	015122	PROSTAGLANDIN ENDOPERO	2.80e-02
	m	107	11.5	602	70	063684	CYCLOOXYGENASE 1.	3.74e-02
	4	107	11.5	602	ព	063921	CYCLOOXYGENASE ISOFORM	3.74e-02
	ហ	105	11.3	347	σ	P76559	FROM BASES 2573751 TO	6.65e-02
	ø	103	11.1	619	۵	023352	HYPOTHETICAL 74.6 KD P	1.18e-01
	7	101	10.8	1584	~	014514	BAI 1.	2.07e-01
	œ	96	10.3	205	12	042394	NISHED (FRAGMENT).	8.25e-01
	0	95	10.2	. 226	σ	006319	HYPOTHETICAL 23.1 KD P	1.08e+00
	10	94	10.1	1337	7	015255	PROTEIN-TYROSINE PHOSP	1.42e+00
	11	93	10.0	469	^	037839	ORF469 PROTEIN.	1.86e+00
	12	93	10.0	1109	7	019179	GUANYLATE CYCLASE E.	1.86e+00
	13	92	6.6	399	유	P97518	ANDROGEN-BINDING PROTE	2.42e+00
	14	92	6.6	399	10	062588	SEX HORMONE-BINDING GL	2.42e+00
	15	92	6.6	833	~	099523	SORTILIN PRECURSOR.	2.42e+00
	16	06	9.7	147	2	061639	3' ORF.	4.11e+00
	17	06	9.7	574	ដ	035298	ACYLOXYACYL HYDROLASE.	4.11e+00
	18	90	9.7	066	œ	040699	LEUCINE-RICH REPEAT/RE	4.11e+00
	19	83	9.6	172	2	061104	FLT3 LIGAND, T169 FORM	5.34e+00
	50	8	9.6	4848	σ	007944	PRISTINAMYCIN I SYNTHA	5.34e+00

6.93e+00 6.93e+00 8.93e+00 8.95e+00 8.96e+00 8.96e+00 1.16e+01 1.16e+01 1.149e+01 1.49e+01 1.49e+01 1.49e+01 1.49e+01 1.49e+01 1.49e+01 1.49e+01 1.49e+01 1.92e+01 1.92e+01 1.92e+01 1.92e+01
NOVEL SERINE PROTEASE. PHENOLOXIDASE (EC 1.10 TIGHT JUNCTION PROTEIN ANION EXCHANGER ISOFOR PCBR. ANION EXCHANGER 2 A (F RIBOSOME RECEPTOR. INTERLEUKIN-3. MAV266 (FRAGMENT). HYPOTHETICAL 30.9 KD P VESICLE COAL PROTEIN S LIM4 PRECURSOR (FRAGME VRG3 PROTEIN (FRAGME VRG3 PROTEIN (FRAGME CTG4A. MRNA (KIAAO081) FOR OR LEUCINE ZIPPER WITH BA PORCINE ZIPPER WITH BA PORCINE MEMBRANE COFAC GLIAL GROWTH FACTOR 2 SEMAPHORIN B. ORF 24. I-ACYL-SN-GLYCEROL-3-P O-POLYMERASE RFC (RFC) LECTITIN.CHOLESTEROL A ADOERZDELTA4-7. MC035R.
092743 0013420 0013420 0055168 0060470 0028334 0028334 0028344 0014696 0014696 0014696 001111 002178 005178 005178 005178 005178 005178 005178
2140004400180224201111111111111111111111
480 111 124 124 1534 1534 1634 1634 1634 1634 1634 1634 1634 16
8 8 8 8 8 8 9 7 7 7 8 8 8 8 8 8 8 9 7 7 7 8 8 8 8
22222222222222222222222222222222222222

ALIGNMENTS

Gaps L11 SEQUENCE FROM N.A. STRAIN-FISCHER 344; TISSUE-TRACHEA; MEDLINE; 95168876. KITZLER J., HILL E., HARDMAN R., REDDY N., PHILPOT R., ELING T.E.; ARCH. BICCHEM. BICCHEM. 316:856-863(1995). EMBL; U18060; G603052; -. SEQUENCE 602 AA; 69032 MW; 7E3888D7 CRC32; EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; RODENTIA. ;; ; DB 10; Length 602; Indels 1 PRELIMINARY; PRT; 602 AA. 60231 60231 60231. 60231. 602731. 602731. 601-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE) 601-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE) PROSTAGLANDIN H SYNTHASE. / Match 11.7%; Score 109; DB 10; Lo Local Similarity 53.6%; Pred. No. 2.09e-02; nes 15; Conservative 6; Mismatches 5; PGHS-1. RATTUS NORVEGICUS (RAT) Query Match Matches RESULT OF STATE OF ST

HOMO SAPIENS (HUMAN). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; PRIMATES. RESULT 2

ID 015122

AC 015122

DT 01-1022

DT 01-102-1996 (TREMBLREL. 01, CREATED)

DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)

DT 01-NOV-1996 (TREMBLREL. 01, LAST SANOTATION UPDATE)

CC EUTHERIA; PRIMATES.

CC EUTHERIA; PRIMATES.

RN [1]

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 90088508.

RA YOKOYAMA C., TANABE T.;

RI BIOCHEM. BIOPHYS. RES. COMMUN. 165:888-894(1989). 12 LLLLLLLPPPPVLLTDAGVPSPVNPCC 39 ద ò

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RESULT

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96 FLAAADGANDASDHIQQMASACRATRLVLGGYSQGAAVIDIVTA-APLPGL-GFTQPLPP 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 02, ANNOTATION UPDATE)
PROTEIN-TYROSINE PHOSPHATASE ETA PRECURSOR (EC 3.11.3.48) (R-PTP-ETA).
                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=H37RV;
MEDLINE; 96181548.
PHILIPP W.J., POULET S., EIGLMEIER K., PASCOPELLA L.,
BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN-TYROSINE PHOSPHATASE ETA. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN-TYROSINE PHOSPHATASE.
                                                                                                                                                                                                                                                                                                                                   Score 95; DB 9; Length 226;
Pred. No. 1.08e+00;
24; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 95086212.
HONDA H., INAZAWA J., NISHIDA J., YAZAKI Y., HIRAI H.;
BLOOD 84:4186-4194(1994).
EMBL; D37781; G633073; --
PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
SIGNAL; GLYCOPROFILIN; TRANSMEMBRANE; REPEAT; HYDROLASE.
SIGNAL:
                               DEVLIN K., CHURCHER C.M.;
SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                           BARRELL B.G., RAJANDREAM M.A., PARKHILL J.;
SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FIBRONECTIN TYPE-III
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                                                                                                                                                                                                                                      COLE S.T.;
PROC. NATL. ACAD. SCI. U.S.A. 93:3132-3137(1996)
EMBL. 295390; E316057; -.
HYDOTHETICAL PROTEIN.
SEQUENCE 226 AA; 23113 MW; C7D17505 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FIBRONECTIN TYPE-II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIBRONECTIN TYPE-II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FIBRONECTIN TYPE-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1337 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                    10.2%;
Local Similarity 27.3%;
hes 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                154 AADDHIAAIALFGNPSG 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
                                                                              SEQUENCE FROM N.A.
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                                                                                              STRAIN-H37RV;
                STRAIN-H37RV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
CARBOHYD
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CARBOHYD
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TRANSMEM
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LT 10
015255
015255;
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01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
NISHED (FRAGMENT).
GALLUS GALLUS (CHICKEN).
EUKARYOTA, METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                     EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                     TIŜSUE-BRAIN;
NISHIMORI H., SHIRATSUCHI T., URANO T., KIMURA Y., KIYONO K.,
TATSUMI K., YOSHIDA S., ONO M., KUWANO M., NAKAMURA Y.;
ONCOGENE 0:0-0(1997).
EMBL, ABO05297; D1024528; -..
SEQUENCE 1584 AA; 173531 MW; 235A5C42 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ë,
                                                                                                                                                                                                                                                                                                                                                                                                 Score 101; DB 2; Length 1584;
Pred. No. 2.07e-01;
3; Mismatches 12; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 KNLPGRAGL-GR-EQFLCPAARRGAGIPQLGHRASGIPRPSPALRASSCS 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.3%; Score 96; DB 12; Length 205; larity 38.0%; Pred. No. 8.25e-01; Conservative 15; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; MYCOBACTERIACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUB-SKELETAL MUSCLE;
DHAR M., MASCARENO E., SIDDIQUI M.A.Q.;
SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF003093; G2232184; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1997 (TREMBLREL. 04, CREATED)
01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
01-JUL-1997 (TREMBLREL. 04, LAST ANNOTATION UPDATE)
HYPOTHETICAL 23.1 KD PROTEIN.
                                                                                                                                            LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 205 AA; 20829 MW; 57AA0342 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             205 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       226 AA
                                                                                             1584 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 WAAVTLLILLIL-PPALLSSGAAAQPLPDCC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 WILAPLILLLIGRRARAAGADAGPGPEPC 43
                                                                                                                             CREATED)
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                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                 10.8%; (ilarity 50.0%; il
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                                                                                              PRELIMINARY;
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MYCOBACTERIUM TUBERCULOSIS.
                                                                                                                        01-JAN-1998 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
                                                                                                                                                                                                          HOMO SAPIENS (HUMAN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 19; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 16; Conser
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SP 656
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102 GA 103
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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006319
006319;
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Gaps

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Gaps
                                                                                                                            PETERSEN C.M., NIELSEN M.S., JACOBSEN L., TOMMERUP N., HOLM H., ROIGAARD H., GLIEMANN J., MADSEN P., MOESTRUP S.K.; SUBMITTED (FEB-1997) TO EMBL/GENBANK/DDBJ DATA BANKS. EMBL; X98248; E246784; -. SIGNAL.
                                                                                                                                                                                                                                                                                                                                                            HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
30 399 SEX HORMONE-BINDING GLOBULIN. 399 AA; 43842 MW; 327FALA7 CRC32;
                                                       Length 399;
                                                   Score 92; DB 10; Length 399
Pred. No. 2.42e+00;
14; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 92; DB 2; Length 833;
Pred. No. 2.42e+00;
4; Mismatches 10; Indels
                                                                                                                                                                                                                                                                01-MAY-1997 (TREMBLREL. 03, CREATED)
01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
SORTILIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33 POTENTIAL.
833 SORTILIN.
92408 MW; D2E351B9 CRC32;
                                                                                                                                                                                                                                      833 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 WPHGLGLLLLLQLLPPSTLSQDRLDAPPP 42
                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 48.3%;
Matches 14; Conservative
                                                  Query Match
Best Local Similarity 33.3%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            833 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
 CHAIN
SEQUENCE
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ID 09
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Search completed: Thu Jul 30 09:04:56 1998 Job time: 50 secs.



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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu Jul 30 09:03:31 1998; MasPar time 5.27 Seconds 623.327 Million cell updates/sec : 0

>US-08-938-548A-2 (1-131) from USO8938548A.pep 931 1 MNLPSIKVSWAAVTLLLLLL......GRRCSAPAAASVAPGGQSGI 131 abular output not generated. Title: Description: Perfect Score: Sequence:

69111 seqs, 25083644 residues PAM 150 Gap 11 Searched:

Scoring table:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

swiss-prot35 1:swiss1

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 41.687; Variance 80.083; scale 0.521

SUMMARIES

Pred. No.	(FR 4.73e-03	2.43e-02	TT 3.36e-02	3P 6.37e-02	3P 6.37e-02	P 8.74e-02	7 1.20e-01	TT 1.20e-01	P 1.64e-01	E 3.04e-01	K 3.04e-01	3P 3.04e-01	m	2.60e-01	Ŋ	P 5.60e-01	P 5.60e-01	7	34 1.37e+00	1.37e+00	1.37e+00	1.37e+00	H 1.37e+00
Description	SECRETIN PRECURSOR (F	TENSIN.	PROSTAGLANDIN G/H SYNT	PROTEIN-TYROSINE PHOSP	PROTEIN-TYROSINE PHOSP	ADENYLATE CYCLASE, TYP	URIDINE KINASE (EC 2.7	PROSTAGLANDIN G/H SYNT	HYPOTHETICAL 22.7 KD	GROWTH REGULATED PROTE	HYPOTHETICAL PROTEIN	PROTEIN-TYROSINE PHOSP	CATION-INDEPENDENT MAN	SL CYTOKINE PRECURSOR	COMPLEMENT C1Q SUBCOMP	TRANS-ACTING TRANSCRIP	TRANS-ACTING TRANSCRIP	STROMELYSIN-3 PRECURSO	SIGNAL TRANSDUCER CD24	E PROTEIN.	LYSIS PROTEIN.	SL CYTOKINE PRECURSOR	HYPOTHETICAL PROTEIN H
Ð	SECR_PIG	TENS_CHICK	PGH1_HUMAN	PTPX_MACNE	PTPX_HUMAN	CYA6_MOUSE	URK1_MOUSE	PGH1_MOUSE	YKO7_YEAST	GRO_CRIGR	Y152_HUMAN	PTPJ_HUMAN	MPRI_BOVIN	FL3L_HUMAN	C1QB_HUMAN	ICPO_HSVBJ	ICPO_HSVBK	COGY_MOUSE	CD24_MOUSE	VGE_BPS13	VGE_BPPHX	FL3L_MOUSE	YCEC_HAEIN
8	Н	-	Н	Н	7	7	П	7	П	Н	П	Н	7	П	П	-	ч	н	Н	-	Н	ч	Н
% Query Match Length	131	1744	599	1013	1015	1165	260	602	205	101	292	1337	2499	235	251	929	9/9	492	16	90	90	232	322
% Query Match	11.5	11.0	10.8	10.6	.10.6	10.5	10.4	10.4	10.3	10.1	10.1	10.1	10.1	6.6	6.6	6.6	6.6	9.8	9.6	9.6	9.6	9.6	9.6
Score	107	102	101	66	66	86	97	97	96	94	94	94	94	92	92	92	92	91	8	8	68	89	89
ult No.	П	7	m	4	2	9	7	∞	<u>ი</u>	10	11	12	13	14	15	16	17	18	19	20	21	22	23

1.37e+00 1.37e+00	1.85e+00	1.85e+00	1.85e+00	1.85e+00	2.47e+00	2.47e+00	2.47e+00	2.47e+00	2.47e+00	2.47e+00	2.47e+00	3.30e+00	3.30e+00	3.30e+00	3.30e+00	3.30e+00	3.30e+00	3.30e+00	4.40e+00	4.40e+00
SERINE PROTEASE SNAKE PHOSPHATIDYLCHOLINE-ST	EPHRIN-A3 PRECURSOR (E	LIPASE 1 PRECURSOR (EC	ADENYLATE CYCLASE, TYP	ADENYLATE CYCLASE, TYP	PROLACTIN PRECURSOR (P	INFECTED CELL PROTEIN	HYPOTHETICAL 36.0 KD P	HFLK PROTEIN.	PROSTAGLANDIN G/H SYNT	LUTROPIN-CHORIOGONADOT	CATION-INDEPENDENT MAN	4-1BB LIGAND (4-1BBL).	TRANSLOCON-ASSOCIATED	WNT-1 PROTO-ONCOGENE P	FIBRIL-FORMING COLLAGE	ATRIAL NATRIURETIC PEP	RETINAL GUANYLYL CYCLA	MULTIDOMAIN VESICLE CO	VERY HYPOTHETICAL 19.8	GPI-LINKED NAD(P)(+)
SNAK_DROME	EFA3_HUMAN	LIP1_PSYIM	CYA6_CANFA	CYA6_RAT	PRL_FELCA	ICP3_HSV1N	YCEC_ECOLI	HFLK_ECOLI	PGH1_SHEEP	LSHR_PIG	MPRI_HUMAN	41BL_HUMAN	SSRA_RABIT	WNT1_MOUSE	CAFF_RIFPA	ANPA HUMAN	CYGD HUMAN	SC16_YEAST	YCX7_YEAST	NARG_MOUSE
	-	 1	Н	Н	-	7	Н	Н	7	Н	Н	7	Н	Н	Н	-	Н	Н	-	-
430	238	317	1165	1166	229	245	319	419	9	969	2491	254	286	370	1027	1061	1103	2194	171	325
0.0 0.0	9.5	9.5	9.5	9.5	9.3	9.3	6.3	6. س	т Э	ь. Э	۳. ص	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.1	9.1
8 8	88	88	88	88	87	87	87	87	87	87	87	98	98	86	86	98	86	86	82	82
22.5	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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TISSUE-PANCREAS;

LIGAGSEB J.W., JELINEK L., SEXSON S., LOFTON-DAY K., BREININGER J.,

SHEPPAND P., KINDSVOGEL W., HAGOPIAN W.A.;

MOL. MED. 3:163-173(1997).

-!- FUNCATION: INPLICATED IN DEVELOPMENT OF NERVOUS SYSTEM AND
PANCREATIC ENDORSHINE CELLS.

-!- CATALITIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)0 =

PROTEIN TYROSINE + ORTHOPHOSPHATE.

-!- SUBCELLULAR LOCATION: TYRO

-!- SUBCELLULAR LOCATION: TYRO

-!- TISSUE SPECIFICITY: PANCREAS.
01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
PROTEIN-TYROSINE PHOSPHATASE X PRECURSOR (EC 3.1.3.48) (R-PTP-X)
(M1851).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTPX_HUMAN STANDARD; PRT; 1015 AA.
092932; 092662.
01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
PROTEIN-TYROSINE PHOSPHATASE X PRECURSOR (BC. 3.1.3.48) (R-PTP-X)
(ISLET CELL AUTOANTIGEN RELATED PROTEIN) (ICAAR) (PHOGRIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- DISEASE: AUTOANTIGEN IN INSULIN-DEPENDENT DIABETES MELLITUS.
-i- SIMILARITY: CONTAINS 1 PROTEIN-TYROSINE PHOSPHATASE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE; 96394649.
CUI L., YU W.-P., DE AIZPURUA H.J., SCHMIDLI R.S., PALLEN C.J.;
                                                                                                                                                                                                                         MACACA NEMESTRINA (PIG-TAILED MACAQUE).
EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA; TETRAPODA; MAMMALLA;
EUTHERIA: PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HOMO SAPIENS (HUMAN).
EUKARYOTA; META2OA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 99; DB 1; Length 1013 Pred. No. 6.37e-02; 7; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 97032784.
KAWASAKI E., HUTTON J.C., EISENBARTH G.S.;
BIOCHEM. BIOPHYS. RES. COMMUN. 227:440-447(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9EC7D263 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BARKER K.T., CROMPTON M.;
TO EMBL/GENBANK/DDBJ DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  111190 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 LLLLLLLPPALLSSGAAAQP 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 LLLLLLLPPRVLPAAPSSVP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 10.6%;
Best Local Similarity 57.1%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           943
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1013 AA;
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-BRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACT_SITE
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                           PTPRN2
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                                STATE THE REPORT OF THE PROPERTY OF THE PROPER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -: SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED. MICROSOMAL MEMBRANE.
-: THIS ENZYME ACTS BOTH AS A DIOXYGENASE AND AS A PEROXIDASE.
-: THIS ENZYME ACTS BOTH AS A DIOXYGENASE AND AS A PEROXIDASE.
-: THIS ENZYME IS THE TARGET OF NONSTEROIDAL ANTI-INFLAMMATORY DRUGS SUCH AS ASPIRIN.
-: ALTERNATIVE PRODUCTS: TWO FORMS CAN BE PRODUCED BY ALTERNATIVE SPLICING OF THE GENE FOR THIS PROTEIN.
-: STMILARITY: CONTAINS I EGF-LIKE DOMAIN.
EMBL: S36211; G249624; -.
EMBL: S36271; G249626; -.
EMBL: S78220; G243972; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CELLS.
-!- CATALYTIC ACTIVITY: ARACHIDONATE + AH(2) + 2 O(2) - PROSTAGLANDIN
                                                                                                                                                                                                                                                                                                                                                                                                            DIAZ A., REGINATO A.M., JIMENEZ S.A.;
J. BIOL. CHEM. 267-110816-10822(1992).
-!- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN REGULATING OR PROMOTING
CELL PROLIFERATION IN SOME NORMAL AND NEOPLASTICALLY TRANSFORMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISTAIR HISTIDINE (BY SIMILARITY).
CYCLOOXYGENASE (BY SIMILARITY).
PROXIMAL HEME LIGAND (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
SAPPIRIN ACCTYLATED SERINE.
S-N: ABOLISH CYLOOXYGENASE ACTIVITY.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00022; EGF_1; FALSE_NEG.
PROSITE; PS01186; EGF_2; FALSE_NEG.
OXIDOREDUCTARE; DIOXYGENASE; PEROXIDASE; GLYCOPROTEIN; ACETYLATION;
PROSTAGLANDIN BIOSYNTHESIS; HEME; IRON; SIGNAL; MEMBRANE;
EGF-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                         TISSUE-PLATELET;
MEDLINE; 92134251.
TAKAHASHI Y., UEDA N., YOSHIMOTO T., YAMAMOTO S., YOKOYAMA C.,
MIYATA A., TANABE T., FUSE I., HATTORI A., SHIBATA A.;
BIOCHEM. BIOPHYS. RES. COMMUN. 182:433-438(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H2 + A + H(2)O.
PATHWAY: FIRST STEP IN THE FORMATION OF PROSTAGLANDINS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 101; DB 1; Length 599
Pred. No. 3.36e-02;
5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MISSING (IN SHORT FORM).
8C7684CD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL. POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 LLFLLLPPLPVLLADPGAPTPVNPCC 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 LLLLLLLLP-PALLSSGAAAQPLPDCC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68656 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.8%;
illarity 51.9%;
Conservative
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE-LUNG FIBROBLAST;
MEDLINE; 92268138.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143
396
599 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
ses 14; Conser
                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THROMBOXANES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ILT 4
PTPX_MACNE
002695;
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DISULFID
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BINDING
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
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SIGNAL DOMAIN

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Gaps

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BANKS

PRT; 1013 AA.

STANDARD;

RESULT ID PT AC 00

Matches

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ETT TET S

Length 1013;

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Gaps

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CRARKENCOSSEEDDIGGE

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ANISOWICZ A., BARDWELL L., SAGER R.;
PROC. NATL. ACAD. SCI. U.S.A. 84:7188-7192(1987).
-!- FUNCTION: HAS CHEMOTACTIC ACTIVITY FOR NEUTROPHILS.
-!- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRICETULUS GRISEUS (CHINESE HAMSTER).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                              VANDENBOL M., BOLLE P.-A., DION C., PORTETELLE D., HILGER F.;
YEAST 10:S35-S40(1994).
EMBL; 228467; G4407501; -.
EMBL; 228146; G486251; -.
PIR; S37804; S37804.
PIR; S44581; S44581.
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 96; DB 1; Length 205; Pred. No. 1.64e-01; 4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |:|: | |||||||||: |::||: | | | | | ::|
PSTKVSWAAVTLILILILPPALLSSGAA-AQPLPDC-CRQKTCSCRL 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 PATR-SLLRAPLLLLLLLLLATSRLATGAPVANELR-CQCLQTMTGVHL 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSF; P09341; IMGS.
PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
CYTOKINE; GROWTH FACTOR; INFLAMMATORY RESPONSE; SIGNAL.
SIGNAL 1 28 POTENTIAL.
                          SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EURARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.1%; Score 94; DB 1; L. Larity 41.7%; Pred. No. 3.04e-01; Conservative 9; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GRO PROTEIN.
BY SIMILARITY.
BY SIMILARITY.
'', 3F83AD41 CRC32;
                                                                                                                                                                                                                                                                                                                                                                    22673 MW; OAEA8D4E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y152_HUMAN STANDARD; PRT; 292 AA. 014165; 01-NOV-1997 (REL. 35, CREATED) 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE) 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE) HYPOTHERICAL PROTEIN KIAA0152. HOMO SAPIENS (HUMAN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 LLLLLLLLLPPLPPVKGEPDAC 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GROWTH REGULATED PROTEIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 GR
63 BY
79 BY
10893 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-1989 (REL. 10, CREATED)
01-MAR-1989 (REL. 10, LAST SEQI
01-DEC-1992 (REL. 24, LAST ANN
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 53.8%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CHEMOKINE CXC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; J03560; G304509; -. PIR; B28414; B28414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 AA;
                                                                                                                                                                                                                                                                                                                                                                       205 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
tes 20; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE; 88041072.
                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                        MEDLINE; 94378720
     OR YKL601
                                                                                                                              STRAIN-S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (C-x-C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRO_CRIGR
P09340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT RESULT OF THE PROPERTY 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
1D Y1
AC Q1
DT Q1
DT Q1
DE HY
GN KI
     셤
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                                                                   01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
PROSTAGLANDIN G/H SYNTHASE 1 PRECURSOR (EC 1.14.99.1) (CYCLOOXYGENASE
-1) (COX-1) (PROSTAGLANDIN-ENDOPEROXIDE SYNTHASE 1) (PROSTAGLANDIN H2
SYNTHASE 1) (PGH SYNTHASE 1) (PGHS-1) (PHS 1).
PTGS1 OR COX1 OR COX-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- SUBUNIT: HOMODIMER.
-1- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED. MICROSOMAL MEMBRANE.
-1- THIS ENZYME ACTS BOTH AS A DIOXYGENASE AND AS A PEROXIDASE.
-1- THIS ENZYME IS THE TARGET OF NONSTEROIDAL ANTI-INFLAMMATORY DRUGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: ARACHIDONATE + AH(2) + 2 O(2) - PROSTAGLANDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN REGULATING OR PROMOTING CELL PROLIFERATION IN SOME NORMAL AND NEOPLASTICALLY TRANSFORMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PSO0002; EGF_1; FALSE_NEG.
PROSITE; PSO1186; EGF_2; FALSE_NEG.
OXIDOREDUCTASE; DIOXIGENASE; PEROXIDASE; GLYCOPROTEIN; ACETYLATION; PROSITALANDIN BIOSYNTHESIS; HEME; IRON; SIGNAL; MEWBRANE; EGF-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE; 90203007.
DEWITT D.L., EL-HARITH E.A., KRAEMER S.A., ANDREWS M.J., YAO E.F.,
ARMSTRONG R.L., SMITH W.L.;
J. BIOL. CHEM. 265:5192-5198(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISTAL HISTIDINE (BY SIMILARITY).
CYCLOOXYGENASE (BY SIMILARITY).
PROXIMAL HEME LIGAND (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (REL. 29, CREATED)
(REL. 29, LAST SEQUENCE UPDATE)
(REL. 30, LAST ANNOTATION UPDATE)
. 22.7 KD PROTEIN IN SDH1-CIMS/YTA3 INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H2 + A + H(2)O.
-1- PATHWAY: FIRST STEP IN THE FORMATION OF PROSTAGLANDINS AND
                                                                                                                                                                                                                              MUS MUSCULUS (MOUSE).
EUKARYOTA, METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSTAGLANDIN G/H SYNTHASE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 97; DB 1; Length 602; Pred. No. 1.20e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASPIRIN-ACETYLATED SERINE.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96489281 CRC32;
602 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUCH AS ASPIRIN.
-1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
EMBL; M34141; G200303; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 WAAVTLILILILIPPALLSSGAAAQPLPDCC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 WFPLLLLLLLPPTPSVLLADPGVPSPVNPCC 39
     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W.
                                                  01-AUG-1991 (REL. 19, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59
71
161
577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A35564; A35564.
HSSP; P01132; 1EGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146
602 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                      EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1994 (REL. HYPOTHETICAL 22.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THROMBOXANES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YKO7_YEAST
P36061;
01-JUN-1994 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1994
01-OCT-1994
PGH1_MOUSE
P22437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
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BINDING

Best Loca Matches

윰 ð RESULT ID YK AC P3 DT 01 DT 01 DE HY

DOMAIN SIGNAL

HSSP;

Gaps

4:

15;

Length 101; Indels

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DSSTLPPPWSPRPLEATA -> VETVFHRVSQDGLDLLTS
                                                                                                                                                                                                                                                                                               ONCOGENE 11:1165-1172(1995).

-1- FUNCTION: STIMULATES THE PROLIFERATION OF EARLY HEMATOPOIETIC CELLS. SYNERGIZES WELL WITH A NUMBER OF OTHER COLONY STIMULATING FACTORS AND INTERLEUKINS.

-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. A SOLUBLE FORM IS ALSO PRODUCED BY ALTERNATIVE SPLICING.

-1- ALTERNATIVE PRODUCTS: VARIOUS FORMS ARE PRODUCED BY ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEMBRANE; ALTERNATIVE SPLICING; SIGNAL
                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE; 94235842.
MEDLINE; 94235842.
MEDLINE; 94235842.
MEDLINE; 94235842.
MOMENT H., SPLETT R.R., BECKMANN M.P., MCKENNA H.J.;
BLOOD 83:2795-2801(1994).
                           SEQUENCE FROM N.A.

MENDLINE; 94195428.

HANDUM C., CULPEPPER J., CAMPBELL D., MCCLANAHAN T., ZURAWSKI S.,
HANDUM C., CULPEPPER J., CAMPBELL D., MCCLANAHAN T., ZURAWSKI S.,
BAZAN J.F., KASTELEIN R., HUDAK S., WAGNER J., MATTSON J., LUH J.,
DUDA G., MARTINA N., PETERSON D., MENON S., SHANAFELT A.,
DUDN G., MARTINA N., PETERSON D., MENON S., SHANAFELT A.,
ZLOTNIK A., RELERF G., NAMMKAWA R., RENNICK D., RONCAROLO M.G.,
ZLOTNIK A., ROSNET O., DUBREUIL P., BIRNBAUM D., LEE F.;
NATURE 368:643-648(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                          MEDLINE; 96032581.
LYMAN S.D., STOCKING K., DAVISON B., FLETCHER F., JOHNSON L.,
ESCOBAR S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SL CYTOKINE.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL) POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (IN ISOFORM E6).
MISSING (IN ISOFORM).
G -> A (IN REF. 1).
F3F8AB35 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 92; DB 1; Len
Pred. No. 5.60e-01;
6; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C1QB_HUMAN STANDARD; PRT; 251 AA. P02746; 21-JUL-1986 (REL. 01, CREATED) 01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE) 01-JUNY-1995 (REL. 32, LAST ANNOTATION UPDATE) COMPLEMENT C1Q SUBCOMPONENT, B CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 86076906.
REID K.B.M.;
BIOCHEM. J. 231:729-735(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M.
                                                                                                                                                                                                                                                                                                                                                                                                           EMBL: U04806; G483845; -.
EMBL: U03858; G494979; -.
EMBL: U29874; G1072037; -.
MIM: 600007; -.
CYTOKINE: GLYCOPROTEIN; TRAN
SIGNAL 27 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.9%;
larity 55.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         235
72
26416 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 AWSPITYLLLLLLSSGL
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235
184
205
235
126
178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CIQB.
HOMO SAPIENS (HUMAN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    235 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
les 10; Consei
    EUTHERIA; PRIMATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE; 86076906.
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loc
Matches
    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
OF THE COMPLEX. THIS RECEPTOR ALSO BINDS INSULIN GROWTH FACTOR II.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. LYSOSOMAL.
-!- DOMAIN: CONTAINS 1S REPEATING UNITS OF APPROXIMATIVELY 147 AA. THE MOST HIGHLY CONSERVED REGION WITHIN THE REPEAT CONSISTS OF A STRETCH OF 13 AA THAT CONTAINS CYSTEINES AT BOTH ENDS.
PIR; A30788; A30788.
PIR; PO2784; 1PDC.
PROSITE; PS00023; FIBRONECTIN_2; 1.
                                                                                                                                                         POTENTIAL.
CATION-INDEPENDENT MANNOSE-6-PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                             ROSITE; PS00023; FIBRONECTIN_2; 1.
RANSMEMBRANE; TRANSPORT; GLYCOPROTEIN; REPEAT; RECEPTOR; LYSOSOME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HOMO SAPIENS (HUMAN).
EURARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 2499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FIBRONECTIN TYPE-II
                                                                                                                                                                                                   LUMENAL (POTENTIAL)
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Pred. No. 3.04e-01;
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu Jul 30 09:02:52 1998; MasPar time 7.57 Seconds 632.140 Million cell updates/sec llar output not generated. m on:

>US-08-938-548A-2 (1-131) from USO8938548A.pep 931 1 MNLPSTKVSWAAVTLLLLLL.......GRRCSAPAAASVAPGGQSGI 131 Title:

Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

120441 segs, 36531193 residues

Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Mean 39.642; Variance 90.062; scale 0.440 pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	1.59e-02	2.13e-02	2.85e-02	2.85e-02	5.09e-02	9.04e-02	1.20e-01	1.20e-01	1.60e-01	1.60e-01	2.80e-01	2.80e-01	2.80e-01	3.70e-01	3.70e-01	4.88e-01	6.43e - 01	6.43e - 01	8.46e-01	1.11e+00	1.11e+00	1.11e+00	1.11e+00
Description P1	prostaglandin G/H syn]	О	secretin precursor - 2	cyclooxygenase 1 - ra	hypothetical protein	sin - chicken (fra 9	sin - chicken 1	tensin, cardiac muscl 1	prostaglandin-endoper 1	prostaglandin-endoper 1	FLT3/FLK2 ligand (clo 2	phogrin - human	transmembrane tyrosin	adenylate cyclase (EC	type 5 adenylyl cycla	prostaglandin-endoper	hypothetical protein (protein	3.4	growth-regulated prot 1		protein-tyrosine-phos 1	mannose 6-phosphate r 1
Desc	S69198 pro	A36746 pro:			A65022 hypo	A57075 tensin	S27939 tensin	0	A38146 pro:		S43293 FLT	JC5062 pho		A46187 ade			S37804 hypo	A61183 hypo	7	4	•		30788 man
DB ID	2 S69	2 A36	1 SEPG	2 \$39	2 A65	2 A57	2 527	2 A5497	2 A38	2 JH0	2 S43	2 305	2 .705	2 A46	2 A49	2 A35	2 537	2 A61	2 JC6	2 B2841	2 I52	1 I38	2 A30
% Query Match Length D	602	599	131	602	347	1792	1733	1744	562	599	245	1015	1015	1165	1166	602	205	31.2	491	101	1337	1337	2499
& Query Match	11.7	11.6	11.5	11.5	11.3	11.1	11.0	11.0	10.8	10.8	10.6	10.6	10.6	10.5	10.5	10.4	10.3	10.3	10.2	10.1	10.1	10.1	10.1
Score	109	108	107	107	105	103	102	102	101	101	66	66	66	86	86	97	96	96	95	94	94	94	94
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S43292 C1HUQB EDBE23 FDBE22	A44399 S24303 A43537	ZEBPF4 JS0455 S47060 I58343	S43291 A49265 G64151 A24702	XXMSN A33141 S28225 S57275	137560 A46180 A47202
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ALIGNMENTS

s preliminary ule_type mRNA ues	A36746 #TYPE complete prostaglandin-endoperoxide synthase (EC 1.14.99.1) 1 #formal_name Homo sapiens #common_name man 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_chan 29-Aug-1997	7	15 LLLLLLLPPALLSSGAAAQPLPDCC	12 LLLLLLLPPPPVLLTDAGVPSPVNPCC	11.7%; Score 109; DB 2; Length 602; Similarity 53.6%; Pred. No. 1.59e-02; 15; Conservative 6; Mismatches 5; Indels 2;	alternative splicing #length 602 #molecular-weight 69032 #checksum	note only a part of the nucleic acid sequence is		#accession S69199	A		Kitzler, J.; Hill, E.; Hardman,	869199	##residues ##cross-references EMBL:U18060: NID:q603051: PID:q603052	##molecule_type mRNA	##status preliminary	*submission submitted to the EMBL Data Library, December 1994 *accession S69198	Kitzler, J.W.	869198	-1997 S69199	OKGANISM #IOTMAI_DAME KATTUS HOLVEGITUS #COMMON_DAME NOTWAY FAT 24-Ang-1996 #segmence revision 13-Mar-1997 #fext Change	prostaglandin G/H synthase 1	S69198 #type complete	RESULT 1
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Occurrence of an actin-inserting domain in tensin.
                                                                                                                                                                                                                                                               Chuang, J.Z.; Lin, D.C.; Lin, S.
J. Cell Biol. (1995) 128:1095-1109
Wolecular cloning, expression, and mapping of the high
affinity actin-capping domain of chicken cardiac tensin.
A57075
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                              15 ILLILILIEPPALLSSGAAAQPLPDCCROKTCSCRLYELLHGAGNHAAGILILGKRRSGPP 74
                                                                                                                                            #type fragment
tensin - chicken (fragment)
#formal_name Gallus gallus #common_name chicken
05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change
10-Sep-1997
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17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
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##residues 862-871,'X',873-875,'A',877-1212 ##label WEI
YY #length 1733 #molecular-weight 186121 #checksum
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submitted to the EWBL Data Library, August 1991
827939
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Pred. No. 9.04e-02;
13; Mismatches 22; Indels
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Pred. No. 1.20e-01;
13; Mismatches 22; Indels
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Best Local Similarity 38.1%;
Matches 24; Conservative
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Best Local Similarity 38.1%;
Matches 24; Conservative
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#authors Diaz, A.; Reginato, A.M.; Jimenez, S.A.
#journal
J. Biol. Chem. (1992) 267:10816-10825.
#title Alternative splicing of human prostaglandin G/H synthase mRNA
and evidence of differential regulation of the resulting
transcripts by transforming growth factor beta 1,
    interleukin 1 beta, and tumor necrosis factor alpha.
#accession A38146
                                                                                                                                                                                          Lo, S.H.; An, Q.; Bao, S.; Wong, W.K.; Liu, Y.; Janmey, P.A.; Hartwig, J.H.; Chen, L.B.
J. Biol. Chem. (1994) 269:22310-22319
Molecular cloning of chick cardiac muscle tensin. Full-length cDNA sequence, expression, and characterization.
A54970
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#formal_name Homo sapiens #common_name man
31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
20-Mar-1999
                  tensin, cardiac muscle - chicken
#formal_name Gallus gallus #common_name chicken
11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change
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#length 1744 #molecular-weight 187256 #checksum 8716
                                                                                                                                                                                                                                                                                                                                                                           preliminary; nucleic acid sequence not shown; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 van de Werken, R.; Gennari, M.; Tavella, S.; Bet, P.; P.; E.; Lin, S.; Cancedda, R.; Castagnola, P. Eur. J. Biochem. (1993) 217-781-790 Modulation of tensin and vimentin expression in chick developing cartilage and cultured differentiating
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##cross-references GB:S36219; NID:g249623; PID:g249624
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11.0%; Score 102; DB 2; I
Best Local Similarity 38.1%; Pred. No. 1.20e-01;
Matches 24; Conservative 13; Mismatches 22;
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#type
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##molecule_type mRNA
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##residues 1469
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##cross-references GB:Y08569; NID:g1644377; PID:e273864; PID:g1644378
T This protein has an intracellular protein tyrosine phosphatase like
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                                    Kawasaki, E.; Hutton, J.C.; Eisenbarth, G.S.
Biochem. Biophys. Res. Commun. (1996) 227:440-447
Molecular cloning and characterization of the human
transmembrane protein tyrosine phosphatase homologue,
phogrin, an autoantigen of type 1 diabetes.
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    #binding_site substrate phosphate (Arg) #status
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#length 1015 #molecular-weight 111366 #checksum 4889
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#binding_site substrate phosphate (Arg) #status
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##residues 1-1015 ##label KAW
##cross-references GB:U66702; NID:g1620663; PID:g1620664
FFICATION #superfamily protein-tyrosine-phosphatase homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##status preliminary; not compared with conceptual translation ##molecule_type mRNA ##molecule_type mRNA ##molecule_type mRNA ##molecule_type mRNA ##molecules 1.1165 ##label YOS ##experimental_source NCB-20 cells ##mote sequence extracted from NCBI backbone (NCBIP:110233) ##mote #superfamily guanylate cyclase catalytic domain homology phosphorus-oxygen lyase; transmembrane protein
                                                                                                                             A46187 #type complete adenylate cyclase (EC 4.6.1.1) type V, calcium-inhibitable
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#domain guanylate cyclase catalytic domain homology
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#label GCC2 #molecular-weight 130318 #checksum 5828
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##note sequence_extracted from NCBI backbone (NCBIN:119384,
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type 5 adenylyl cyclase - mouse
#formal_name Mus musculus #common_name house mouse
19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change
07-Jul-1995
                                                                                                                                                                                                                                                                                                                                                              ERENCE A46187

#authors Yoshimura, M.; Cooper, D.M.

#journal Proc. Natl. Acad. Sci. U.S.A. (1992) 89:6716-6720

#title Cloning and expression of a Ca(2+)-inhibitable adenylyl

#cross-references MUID:92357702
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16-Feb-1997
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    148 SSLTLLMAVLVLLMAVLLTFHAAPAQPQPAYVALLTCASVLFVVL 192

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##molecule_type nucleic acid
##residues 1-1166 ##label PRE
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

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Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

63816 seqs, 5850866 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

a-issued 1:5_COMB 2:PCT9_COMB 3:backfiles Database:

Mean 27.627; Variance 133.583; scale 0.207 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Pred. No.	4.75e+00	6.53e+00	6.53e+00	7.65e+00	7.65e+00	1.05e+01	1.05e+01	1.05e+01	1.05e+01	1.23e+01	1.23e+01	1.23e+01	1.68e+01	1.96e+01	2.29e+01	2.29e+01							
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& Query Match	10.1	9.9	6:6	9.6	9.6	9.6	9.6	9.6	9.6	9.5	9.5	9.5	9.5	9.1	9.1	9.1	9.1	9.1	9.1	9.1	9.1	9.0	0.6
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Length 1337;

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Query Match

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		0 HH		m רו ר	1			STANDARD;		ication PC,	lication PC	ATION: Tonks, Nich	TITLE OF INVENTION: DE	QUENCES: (Marshall, Borun	33 South Wa	Illinois	United States 6	MEDIUM TYPE: Floppy	IBM PC COMPATIBLE SYSTEM: PC-DOS/MS	CURRENT APPLICATION DATA:	N NUMBER:	NT INFORMAT un, Michael	REGISTRATION NUMBER: 2 REFERENCE/DOCKET NUMBER	TELECOMMUNICATION INFORMATION: TELEPHONE: 312-474-6300	312-474-044 R SEQ ID NO	SEQUENCE CHARACTERISTIC LENGTH: 1337 amino a	linear	1, 146192
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24 82 25 82 26 82 27 81	28 81 229 81 30 80 31 80	O1 00 47 E	200	യത	5 H M	w 4∗r∪		1 CT-US95	XXXXXX	Sequence	Sequence	GENERA	TITL	NUMB	A	ST	ST	200	COMP	88	CURR	FI	ATTO	RE	TELE	TE INFORM	SEOG	MOLE	SEQUENCE
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Sequence 4, Application US/07794393
Patent No. 5236844
GENERAL INFORMATION: APPLICANT: CHAMBON, PIERRE
APPLICANT: BASSET, PAUL
APPLICANT: BELLOCQ, JEAN-PIERRE
TITLE OF INVENTION: CANCER
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: 4
CORRESPONDENCE ADDRESS: 5
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1225 Connecticut Ave. NW Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 9.8%; Score 91; DB 1; Length 492; Best Local Similarity 47.6%; Pred. No. 7.65e+00; Matches 10; Conservative 9; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/794,393
FILING DATE: 19911121
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9025326.1
FILING DATE: 21-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAMME: GOLDSTEIN, JORGE A
REGISTRATION NUMBER: 29,021
REFERENCE/POCKET NUMBER: 29,021
REFERENCE/POCKET NUMBER: 1383.0040000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         231 AA.
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JENCE 492 AA; 55340 MW; 1261070 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                   PRT;
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                                                                                                                                                                     Sequence 4, Application US/07794393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (202) 833-8716 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Washington STATE: D.C.
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ZIP: 20036
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                                                LT 5
US-07-794-393-4
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Patent No. 548476
GENERAL INFORMATION:
APPLICANT: BASSET, PAUL
APPLICANT: BLACCO, UBAN-PIERRE
APPLICANT: CHAMBON, PIERRE
TITLE OF INVENTION: ANALYTICAL MARKERS FOR MALIGNANT BREAST
TITLE OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                                Score 92; DB 2; Length 235;
Pred. No. 6.53e+00;
6; Mismatches 2; Indels
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9.8%; Score 91; DB 1; Length 492;
Best Local Similarity 47.6%; Pred. No. 7.65e+00;
Matches 10; Conservative 9; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Sterne, Kessler, Goldstein & Fox STREET: 1225 Connecticut Suite 300
CITY: Washington
STATE: D.C.
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SPETANTON TANDER: US/08/001,711
FILING DATE: 19930107
                                                                                                                                                                                                                                       492 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: MILLMAN, ROBERT A REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 1383.0040001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/794,393
FILING DATE: 11-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9025626.1
FILING DATE: 21-NOV-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
JENCE 492 AA; 55340 MW; 1261070 CN;
               MOLECULE TYPE: protein
JENCE 235 AA; 26415 MW; 293990 CN;
                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08001711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (202)833-8716
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 492 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 LLLLLLLPSPLMARARPPES 42
                                                                                                                                                                                                                                       STANDARD;
                                                              Query Match 9.9%;
Best Local Similarity 55.6%;
Matches 10; Conservative
                                                                                                                                                     9 SWAAVTLILLLIPPAL 26
                                                                                                                                  7 AWSPITYLLLLLLSSGL 24
TOPOLOGY: linear
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CLASSIFICATION:
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US-08-001-711-4
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ij
                               APPLICANT: Nocka, Karl (US only)
APPLICANT: Lobell, Robert B (US only)
TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND AND
TITLE OF INVENTION: FLI-3/FLK-2 LIGAND
NUMBER OF SEQUENCES: 36
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                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03866
CytoMed, Inc. (all states except US)
Nocka, Karl (US only)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   238 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Mismatches
                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
PRIOR PAPLICATION:
PRIOR PAPLICATION:
APPLICATION NUMBER: US 08/220,379
FILING DATE: 28-MAR-1994
ATTORNEY AGENT INFORMATION:
NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: CytoMed/2
                                                                                                                                                                                                                                                                                                                                       United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 9.6%; Score 89; I
Best Local Similarity 57.9%; Pred. No. 1.
Matches 11; Conservative 5; Mismatc
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LOCATION: 1..205
ICE 231 AA; 25999 MW; 274601 CN;
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Patent No. 5516658
GENERAL INFORMATION:
APPLICANT: BECKMAN, M. P.
APPLICANT: CERRETII, DOUGLAS P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08240124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 212-550 INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
TWATH: 231 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 AWSPNSSLLLLLLLLSPCL 25
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                                                                                                                                                                                                                                                                                                                                       COUNTRY: UN
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                                                                                    APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
WUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEB: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 231;
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                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,545
FILING DATE: 11-MAY-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         231 AA
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/162,407
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
CLASSIPICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
CLASSIPICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: MAY 24, 1993
CLASSIFICATION: A35
ATORNEY/AGENT INFORMATION:
NAME: MAIDER: SEPHEND:
RESISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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JENCE 231 AA; 26027 MW; 272421 CN;
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Sequence 2, Application US/08243545
Patent No. 5554512
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (206) 587-0430
(206) 233-0644
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 231 amino acids
amino acid
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ilarity 57.9%;
Conservative
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                                                                                                                                                                                                                                                                                                                                       Washington : US
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Best Local Similarity
Matches 11; Conserv
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STANDARD;
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OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                 Query Match 9.2%;
Best Local Similarity 61.1%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                 S VSWAAVTLLLLLLLPPA 25
                                                                                                                                                                                                                                                     27 LPWALVAGLLLLLLLAAA 44
                                                                                                                                                                                                                                                                                                                                                                           RESULT 14

AC XXXXX

AC XXXXXX

DE Sequence 170, Applic XX Color Applicant Color Color Applicant Color Applicant Color Color Applicant Color A
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CITY: Seattle
STATE: Washington
VUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Alderson, Mark R.
APPLICANT: Goodwin, Raymond G.
APPLICANT: Smith, Craig A.
TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 88; DB 1; Length 1165
Pred. No. 1.23e+01;
14; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    148 SSLTLLMAVLVLLTAVLLAFHAAPARPQPAYVALLACAATLFVAL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 AAVTLLL-LILLIDPPALLS-SGAAAQPLPDCCRQKTCSCRLYELL 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      254 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple 7.5.3
SOFTWARE: Microsoft Word, Version #6.0.1
CURRENT APPLICATION DATA:
FILLING DATE: 06-May-1994
                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
FENCE 1165 AA; 130394 MW; 6766222 CN;
APPLICATION NUMBER: US/08/240,357
FILING DATE: 10-MAY-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/060,843
FILING DATE: 07-May-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/08236918A
Patent No. 5674704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08236918A
                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Gordon, Alan M.
REGISTRATION NUMBER: 30,637
REFRENCE/DOCKET NUMBER: 31,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-831-3244
                                                                                                                             30,637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,17
REFERENCE/DOCKET NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (206) 587-0430
                                                                                                                                                                                                                            TELEFAX: 201-831-3305
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1165 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                       201-831-3305
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 9.5%;
Local Similarity 33.3%;
les 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS: ADDRESS:
                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                    ropology: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 07 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-236-918A-4
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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88888888888888888888888888

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APPLICANT: Goodearl, Andrew; Stroobant, Paul;
APPLICANT: Goodearl, Andrew; Stroobant, Paul;
APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
APPLICANT: Chen, Maio Su; Hiles, Ian
TITLE OF INVENTION: Glial Mitogenic Factors, Their
TITLE OF INVENTION: Preparation and Use
NUMBER OF SEQUENCES: 184
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York City
STATE: New York
COUNTY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                        Score 86; DB 1; Lengtn 2...
Pred. No. 1.68e+01;
Pred. "...+rhes 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        422 AA
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CURRENT APPLICATION DATA:
APPLICATION NOMBER: US/08/469,569
FILING DATE: 06-JUN-1995
CLASSIFICATION NAMBER: US/086,559
FILING DATE: 24-MAR-1993
APPLICATION NUMBER: 07/965,173
FILING DATE: 23-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/940,389
FILING DATE: 30-OWN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/907,138
FILING DATE: 30-UWN-1992
FILING DATE: 30-UWN-1992
FILING DATE: 30-UWN-1992
FILING DATE: 30-UWN-1992
FILING DATE: 03-SPRICATION DATA:
APPLICATION NUMBER: 07/863,703
FILING DATE: 03-SPRICATION DATA:
APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 10-APRIL-1991
ATTORNEY/AGENT INFORMATION:
RAME: Tsai, Christine H.
REGISTRATION NUMBER: 34,266
REPERENEL/COCKET NUMBER: LUD 5250.4
TELECOMMUNICATION:
TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
LENGTH: 254 amino acids
TYPE: amino acid
TYPE: 11near
TOPOLOGY: 11near
MOLECULE TYPE: protein
SEQUENCE 254 AA; 26624 MW; 316872 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 170, Application US/08469569
Patent No. 5606032
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 170, Application US/08469569
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(MI)

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protein - protein database search, using Smith-Waterman algorithm MPsrch pp

Thu Jul 30 09:02:10 1998; MasPar time 5.32 Seconds 377.841 Million cell updates/sec on:

rabular output not generated. Title:

>US-08-938-548A-2 (1-131) from US08938548A.pep 931 1 MNLPSTKVSWAAVTLLLLLL......GRRCSAPAAASVAPGGQSGI 131

Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

124785 segs, 15338987 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

a-geneseq31-2 Database:

| part| 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part27

Mean 29.691; Variance 135.127; scale 0.220 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

)		dР					
Result	9100	Query	Tongth DR	2	· F	00001101	or or or
	2070	Ma CC11		3 !		Description	
	108	11.6	599	4	R21690	Prostaglandin endoper	1.04e+00
7	66	10.6	696	24	W25170	Human insulinoma-asso	4.77e+00
٣	66	10.6	986	24	W25171.	Human insulinoma-asso	4.77e+00
4	66	10.6	1012	56	W35296	Macaque islet cell an	4.77e+00
S	66	10.6	1015	27	W35345	Human protein tyrosin	4.77e+00
ø	66	10.6	1015	23	W18092	Type I diabetes assoc	4.77e+00
7	94	10.1	1337	14	R85203	hudep-1.	1.09e+01
œ	92	9.9	235	12	R67541	Human flt-3 ligand.	1.52e+01
6	92	9.9	235	13	R66175	Human S86/S109 Flt3 1	1.52e+01
10	91	9.8	492	Ŋ	R24863	Sequence of pre-pro s	1.78e+01
11	88	9.6	35	Н	P94256	Truncated E protein f	2.47e+01
12	89	9.6	231	12	R67540	Mouse flt-3 ligand.	2.47e+01
13	89	9.6	232	13	R66177	Mouse MoT110/T118 Flt	2.47e+01
14	88	9.5	234	16	R82605	Eph transmembrane tyr	2.90e+01
15	88	9.5	238	13	R71481	Human hek-L protein.	2.90e+01
16	88	9.5	480	23	W22849	Osteoblast like cell	2.90e+01
17	88	9.5	1165	^	R37309	Cardiac adenylyl cycl	2.90e+01
18	87	9.3	186	9	R32428	Wheat germ agglutinin	3.40e+01
19	87	9.3	551	13	R77858	S. clavuligerus ORF1	3.40e+01

3.40e+01 3.99e+01	3.99e+01	3.99e+01	3.99e+01	4.68e+01	4.68e+01	4.68e+01	4.68e+01	4.68e+01	4.68e+01	4.68e+01	4.68e+01	4.68e+01	4.68e+01	4.68e+01	4.68e+01	4.68e+01	4.68e+01	4.68e+01	4.68e+01	4.68e+01	5.49e+01	5.49e+01	5.49e+01	5.49e+01
Prostaglandin endoper ICP34.5 fraqment.	Human 4-1BB ligand.	Human 4-1BB-L polypep	rchd528 gene product.	cell g	growt	glial	GGF segment E.		GGF segment E.	Porcine complement in	Human glial cell grow		GGF-II encoded by clo	Glial growth factor s	Mature hGGF2.	Human GGF2.	Glial growth factor s	Glial growth factor G	GGF-II encoded by clo	C. acidovorans stereo	Murine interleukin-15	Insulin-like growth f	Wzy (Rfc) protein inv	Human DOCK180 protein
P91008 R50054	W26657	R64190	W03740	R67242	W09358	R87445	R55653	R96074	R46912	W12414	R67258	W09371	R46923	R87467	R86628	W09372	R87466	R96081	R55654	R31036	R90840	R89952	W37355	W03515
~ &	25	12	13	12	21	16	0	11	σ	23	17	21	σ	16	16	21	16	11	σ	φ	16	15	27	13
600 126	254	254	1481	248	248	248	248	248	248	363	422	422	422	422	422	422	422	422	422	426	263	291	438	1865
6.6 6.7	•	٠	9.5	9.1	•	9.1	9.1	9.1	9.1	9.1	9.1	6.7	9.1	9.1	6	9.1	9.1	.9.1	9.1	9.1	0.6	0.6	0.6	9.0
	98								82							82	82	82	82	82	84	84	84	84
20	22	23	24	25	26	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

The protein sequence of hPES was deduced from the cDNA sequence obtd. by screening a human genomic library in EMBL3. hPES can be used to screen arti-inflammatory agents. An anti-body against a peptide specific to hPES can be made, and used for the determination of the protein.

Sequence 599 AA; Human prostaglandin endo-peroxide synthase - for screening antiinflammatory agents Claim 1; Page 1; 10pp; Japanese. Prostaglandin endoperoxidé synthase. Human: hPES; screening; anti-inflammatory; antibody. Homo sapiens. J040465786-A. r R21690 standard; Protein; 599 AA. 14-FEB-1992. 13-JUN-1990; 152784. 13-JUN-1990; JF-152784. (MEIP.) MELJI MILK PRODS KK. WPI; 92-101937/13. R21690; 23-JUL-1992 (first entry) N-PSDB; Q23001 RESULT

Gaps ü Length 599; 7; Indels Score 108; DB 4; Pred. No. 1.04e+00; 4; Mismatches Query Match
Best Local Similarity 55.6%;
Matches 15; Conservative

ij

10 lllllllpplpvlladpgaptpvnpcc 36 15 LLLLLLLP-PALLSSGAAAQPLPDCC 40 윱 ò

.r 2 W25170 standard; Protein; 969 AA.

W25170; 15-DEC-1997 (first entry) Human insulinoma-associated antigen 2-beta (short version). Insulinoma-associated antigen 2 beta; IA-2 beta; autoantigen; insulin dependent diabetes; IDD; antibody; diagnosis; susceptibility;

type 1; type 2. Homo sapiens. WO9707211-A1.

Domain Domain Domain

Region

```
Novel islet cell antigen-related protein tyrosine phosphatase resequising auto-antibodies associated with insulin useful for recognising auto-antibodies associated with insulin dependent diabetes mellitus

Claim 4: Page 57-63; 67pp; Brajish.

Human islet cell antigen-related protein tyrosine phosphatase

CI (RR-PRP) (WI8092) has the properties of an insulin-dependent

Ci (RR-PRP) (WI8092) has the properties of an insulin-dependent

Ci (AR-PRP) (WI8092) has the properties of an insulin-dependent

Ci (AR-PRP) (WI8091) and color co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Page 34-38; Sipp; English.
A cDNA clone was obtd. (see T06027) from a HeLa cell cDNA library that encoded a novel density-enhanced Type III receptor-like PTP, designated hubEp-1 (R85203). hubEp-1 is useful for the study of PTPs and for the development of therapeutic or prophylactic cpds. e.g. for prevention of abnormal or malignant cell growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Density enhanced Type III receptor-like protein tyrosine phosphatase;
hubBP-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New density enhanced protein tyrosine phosphatase - used to develop prods. to modify transcription, translation and/or activity of tyrosine phosphatase(s).
                                                                                                                                                                                                                                                                                                                                                                                          /label- Glycosylation
/note- "potential N-linked glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.6%; Score 99; DB 23; Length 1015;
larity 57.1%; Pred. No. 4.77e+00;
Conservative 7; Mismatches 2; Indels (
                                                                                                     22.614
/label= Extracellular_domain
                                                                                                                                                                           615..639
/label- Transmembrane_domain
                                                                                                                                                                                                                                                640..1015
/label= Intracellular_domain
label Sig_peptide
                                                                     /label- Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R85203 standard; Protein; 1337 AA.
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03-MAY-1995.
03-MAY-1994; US-237940.
(COLD-) COLD SPRING HARBOR LAB.
OSSTHAM A, TONKS NK;
WPI: 95-393079/50.
N-PSDB: T066027.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-DEC-1995; GB-026036.
19-MAR-1996; GB-005710.
27-SEP-1996; GB-020265.
(UXSI-) UNIV SINGAPORE NAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-FEB-1996 (first entry) hubEP-1.
                                ..1015
                                                                                                                                                                                                                                                                                                                     942..954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
tes 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-JUN-1997.
20-DEC-1996; CA0867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 97-341685/31.
N-PSDB; T67296.
                                                                                                                                                                                                                                                                                                                         active_site
modified_site
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WO9530008-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09722694-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pallen CJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                        protein
                                                                                                             domain
                                                                                                                                                                                                                                                       domain
                                                                                                                                                                                  domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein tyrosine phosphatase, designated MOT12, suggested to play a role in the growth, differentiation and survival of neurons in the adult. The amino acid sequence was deduced from a coding sequence (see 19388) of overlapping cDNA clones isolated from human caudate nucleus and pancreas cDNA libraries. MOT12 expression is highly restricted, being found only in adult brain and pancreas in neurosecretory cell types. Polypeptides, including those that comprise residues 1-614, 615-706 or 707-1082 of MOT12 or comprise MOT12 lacking one or more of the extracellular, transmembrane or intracellular domains, can be expressed in host cells. The MOT12 polypeptides, nucleic acids encoding them, cells, tissues, transgenic animals and antibodies can be used in methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 97-503042/46.
WPI; 97-503042/46.
WPISDB; T95368.
Protein tyrosine phosphatase MOT12 - used to develop products for the diagnosis and treatment of, e.g. cell proliferative disorders, diabetes and immune disorders
Claim 9; Fig 1; 64pp; English.
This protein sequence comprises a novel human receptor-type
This protein sequence comprises a novel human receptor-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WI8092;
14-SEP-1997 (first entry)
Type I diabetes-associated autoantigen IAR-PTP.
Insulin dependent diabetes mellitus-associated autoantigen; IDDM;
islet cell antigen-related protein tyrosine phosphatase; IAR-PTP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for the treatment, diagnosis and screening of MOT12-related diseases or conditions characterised by an abnormal interaction between MOT12 and a natural binding partner, especially diabetes an immune disorder or cancer (claimed).
                                                                                                                                                                                                                                                                                                              /note- "residue 294 is Glu in protein encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "predicted phosphotyrosine contact site" 776..779
                                                                                                                                                                                                                                                                                                                                                                                                                               note- "predicted phosphotyrosine contact site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note- "predicted base of binding pocket"
911..919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "predicted rim of binding pocket"
951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "predicted surface loop"
                                                                                                                                                                                                                                                                                                                                                      a pancreas cDNA clone"
                                                                                                                               615..706
/note= "transmembrane domain"
                                                                                                                                                                                                        707..1082
/note= "intracellular domain"
                                                                                                  "extracellular domain"
                                    Location/Qualifiers
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                                                                        1..614
/note=
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25-MAR-1997; US-816962.
29-MAR-1996; US-014267.
                                                                                                                                                                                                                                                                                    Misc_difference 294
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Matches 12; Conser
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       Homo sapiens.
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Query Match

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National Market National Natio
                                                                                                                                                    Isolated ligands for flt 3 receptors - useful for treating anaemia, AIDS and various cancers Disclosure; page 25-27, 33pp, English.

CDNA encoding mouse flt3-ligand (flt3-L) was isolated from a CDNA network of T-cell line P7B-0.3A4 in CV-1/EBNA-1 cells using a slide autoradiography method. Flt3-L stimulates production of progenitor and stem cells, and can be used e.g. Sequence 231 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 9.6%; Score 89; DB 13; Length 232; Best Local Similarity 57.9%; Pred. No. 2.47e+01; Matches 11; Conservative 5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 231;
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Pred. No. 2.47e+01;
5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-AUG-1995 (first entry)
Mouse MoT110/T118 Flt3 ligand peptide fragment.
Flt3 ligand; tyrosine kinase receptor ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Birnbaum D, Culpepper JA, Hannum CH, Lee FD; WPI; 95-006787/01.
N-PSDB; Q79464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 NOV-1994; U05150.
18-MAY-1994; U05150.
19-MAY-1993; US-065231.
07-JUL-1993; US-089263.
16-UL-1993; US-106340.
24-AUG-1993; US-112391.
19-NOV-1993; US-155111.
03-DEC-1993; US-155111.
(INRW ) INST NAT SAWTE & RECH MEDICALE.
(SCHE ) SCHERING CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R66177 standard; Peptide; 232 AA.
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Best Local Similarity 57.9%;
Matches 11; Conservative
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                                                      Beckmann MP, Lyman SD;
WPI; 95-008071/02.
N-PSDB; Q79076.
                              (IMMV) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
11-MAY-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Treating or preventing microbial infections - using cecropin(s), attacin(s), lysozyme(s), S protein from lambda phage, E protein from pHi x174 or protein from phage 22.

Claim 108; page 58; 64pp; English.

The truncated E protein is an antimicrobial polypeptide. DNA encoding the protein is used to transform animal cells to express the protein, proteins may also be admin. to humans and animals for preventing or transforms, eg brucellosis, malarial infection. The proteins and Chagas disease.

See also P94254-P94258.
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06-JUL-1987; US-069653.
(LOUT) Louisiana State University Agricultural and Mechanical College.
Jaynes JM, Enright FM, White KL;
WPI: 89-039653/05.
                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse fit-3 ligand. Fit-3 ligand, fit3-L; anemia; cancer; AIDS; gene therapy.
                           Length 492;
                                                                                           2; Indels
                       Score 91; DB 5; L/
Pred. No. 1.78e+01;
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/label- Transmembrane_domain
                                                                                           Mismatches
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/label- Cytoplasmic_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-JUN-1990 (first entry)
Truncated E protein from Phix174.
E protein; antimicrobial agent; Phix174.
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28..188
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R67540: standard; Protein; 231 AA.
R67540:
05-AUG-1995 (first entry)
                                                                                                                                                                                                                                                                                                                              JT 11
P94256 standard; protein; 35 AA
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Best Local Similarity 55.6%;
Matches 10; Conservative
                           Ouery Match
Best Local Similarity 47.6%;
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10 WAAVTLLLLLLLLPPALL 27
                                                                                              10; Conservative
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US-106463.
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US-209502.
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                                                                                                                                                                                                                                                                                                                                                                                           P94256;
10-JUN-1997
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07-MAR-1994;
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu Jul 30 09:33:36 1998; MasPar time 3.35 Seconds 128.334 Million cell updates/sec bular output not generated. no un

>US-08-938-548A-12 (1-28) from US08938548A.pep 201 1 RPGPPGLQGRLQANGNHAAGILIM 28

Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

124785 seqs, 15338987 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

1.part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part22 23:part25 26:part26 27:part27 a-geneseq31-2 Database:

Mean 22.110; Variance 87.356; scale 0.253 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		dР					
Result No.	Score	Query	Length DB	DB	q	Description	Pred. No.
П	89	33.8	2192	23	W21732	LexA/NuMA fusion prot	4.36e+01
~	99	33.8	2272	23	W21731	GAL4/HA/NuMA fusion p	4.36e+01
m	99	32.8	10	4	R20235	"p33" N-terminal (2).	6.36e+01
4	9	32.3	716	18	R99737	Retinoid X receptor i	7.68e+01
S	65	32.3	2509	54	W32881	Protein (OA-519) cros	7.68e+01
9	64	31.8	256	σ	R45403	Deduced sequence of h	9.25e+01
7	64	31.8	256	15	R85639	MY17 preproPR-3.	9.25e+01
80	64	31.8	549	16	R92050	KM31-7 precursor.	9.25e+01
σ	64	31.8	1477	13	R67691	S. cerevisiae scaur2R	9.25e+01
10	64	31.8	1477	55	W10424	Saccharomyces cerevis	9.25e+01
	63	31.3	878	Q	R32889	DHR23alpha protein.	1.11e+02
12	63	31.3	878	ო	R13793	Ecdysone receptor.	1.11e+02
13	63	31.3	1841	25	W22605	Tylactone synthase OR	1.11e+02
14	63	31.3	4630	22	W19629	Streptomyces venezuel	1.11e+02
15	62	30.8	684	24	W26327	Human alpha-1 collage	1.34e+02
16	19	30.3	32	Н	R00579	New polypeptide based	1.61e+02
17	61	30.3	248	ч	R04216	Human 32K ASP encoded	1.61e+02
18	61	30.3	248	7	P82980	Sequence deduced from	1.61e+02
19	61	30.3	248	m	P60666	Genomic sequence of h	1.61e+02

0000	00000	00000	1000000	
61e+02 61e+02 61e+02 61e+02	61e+02 61e+02 61e+02 61e+02 61e+02	.61e+02 .61e+02 .61e+02 .93e+02	. 936+02 . 936+02 . 936+02 . 936+02	.93e+02 .93e+02 .93e+02 .93e+02 .93e+02
11.62	96999	99999		
ed on	rfac rfac alv (10)	t p q q	n-11 15 in 10 in 11 in f IL-	fus fus pro hea on
V(10 surf ncod	surfac surfac lan alv SV(10)	lar e of incoc	ם ישיים	IL-11 fudes-Pro- lated pr ticus he sociated
Pc-S lar SP e duce	nary surfa nary surfa f human al SPcq-SV(10 35K-1A-10	lvec uenc SP e gene	leuk leuk gene leuk ein	-IL- /des elat atic ssoc
pAS lveo 2K A e de	pulmonary pulmonary ince of hum iid pASPcq-	32K alveolar su c sequence of h 32K ASP encoded adipogenesis in	interleukin-11 interleukin-11 adipogenesis i Interleukin-11 protein of IL	oxin oxin as-r aqu ce-a
Plasmid pASPc-SV(10) Human alveolar surfac Human 32K ASP encoded Sequence deduced from	35kd pulmonary surfac 35kd pulmonary surfac Sequence of human alv Plasmid pASPcq-SV(10) Vector PSP 35K-1A-10			Thioredoxin-II-II fus Thioredoxin-II-II fus Thioredoxin/des-Pro-I Human Ras-Telated pro Thermus aquaticus hea Virulence-associated Human focal adhesion
Pla Hum Hum Seg	35kd 35kd Seque Plasm Vecto	Human Genomj Human Human	Human Human Human Human Fusion	Thi Thi The The
P60441 R06331 R04215 P80694	P70662 P70663 P60665 P60442 R05091	R04212 P60661 R04217 R43261	R43260 R43260 R50176 R26213	R75762 R75762 W00084 R49835 R76480
P6044 R0633 R0421 P8069	P70 P70 P60 P60 R05	R04 R04 R43	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	R7576 W0008 R4983 R4983 R7648
кччч	00000	чкч ва	'AA' A''	
248 248 248	248 248 248 248 248	271 271 271 271 169	11111 2000 1000 1000 1000	296 296 296 405 510 530
	m m m m m			
3000	30.3 30.3 30.3 30.3 30.3	28999	0000000	0000000
55555	61111	1 H H O O	000000	0000000
222	24 25 27 28	33733	4500000	044444

ALIGNMENTS

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4 rppspalasvllalllsgaaraaeiv 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 31.8%;
Best Local Similarity 38.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
 processing.
Sequence 256 AA;
                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                W09524501-A1
                                                                                                                                                                                                                                                                                                                                 peptide
                                                                                                                                                                                                                                                                                                                                                           peptide
                                                                                                                                                                                                                                                                                                                                                                                      protein
                                                                                                                                                                                              R85639;
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ID R9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                          DNA encoding protein cross-reactive with hpr gene product - useful to raise antibodies reactive with epitope(s) found on hpr gene product, useful in cancer, especially breast cancer, prognosis
                                                                                                                                                                                                                                                                                                                                                              ဍ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        culture media in which it is grown). The convertase produced by HL60 has been sequenced and is identical to the known lymphocyte serine protease PR-3 which has other activities unrelated to INF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cpds. which inhibit formation of mature tumour necrosis factor from its precursor - identified using TNF convertase, e.g. mutain(s), antibodies or peptide phosphonate(s), for preventing and treating sepsis, AIDS, auto-immune disease etc. Disclosure; Fig 2; 69pp; English.
                                                                                                                                                                                                                                                                                                                                Claim 2; Columns 43-60; 68pp; English.#
The present sequence is a protein (OA-519) cross-reactive with the haptoglobin related (hpr) gene product. OA-519 can be used raise antibodies reactive with epitopes found on the hpr gene product, but not on haptoglobin 1 or 2, useful in cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
         Protein (OA-519) cross-reactive with hpr gene product.
OA-519; cross-reaction; haptoglobin related; hpr; antibody;
epitope; haptoglobin 1; haptoglobin 2; cancer; breast cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-JUL-1994 (first entry)
Deduced sequence of human proteinase-3 (PR-3)
TNF convertase; proteinase-3; PR-3; tumour necrosis factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-JAN-1994.
25-JUN-1993; U06120.
25-JUN-1992; US-905546.
(CETU) OCETUS ONCOLOGY CORP.
Halenbeck RF, Jewell DA, Koths KE, Kriegler M, Perez C;
WPI; 94-026195/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2509;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 32.3%; Score 65; DB 24; Length 250
Best Local Similarity 29.6%; Pred. No. 7.68e+01;
Matches 8; Conservative 10; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   especially breast cancer, prognosis assays. Sequence 2509 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 411 ppapaphatlprllrasgrtpeavqkl 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 PGPPGLQGRLQRLLQANGNHAAGILIM 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R45403 standard; Protein; 256 AA.
                                                                                                                                                                            24-JUL-1992; US-917716.
26-JUL-1993; US-916908.
05-JUN-1995; US-469008.
(UVJO ) UNIV JOHNS HOPKINS.
Kuhajda FP. Pasternack GR;
WPI: 97-469516/43.
N-PSDB; T88206.
                                                                                                                                                     US-622407
                                                       proquosis assay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; Q54498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
WO9400555-A.
                                                                     Homo sapiens.
                                                                                                                                                    04-DEC-1990;
26-JUL-1991;
                                                                                                            17-JAN-1989;
                                                                                                                                        17-JAN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R45403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
셤
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treatment of septic shock, Theumatoid arthritis, From.

Example 2; Page 82; 96pp; English.

Chis sequence represents the preproper 3. PR-3 is active recombinant human neutrophil protease-3. PR-3 is a scrine protease, and is a tumour neutrophil protease-3. PR-3 is a scrine protease, and is a tumour neutrophil protease-3. PR-3 is a scrine protease, and is a tumour necrosis factor alpha (TNFalpha) convertase. The cDNA encoding this conscribed from the HL60 cell clone MX17. The mature PR-3 can be used in the method of the invention for identifying agents that the method of proTNFalpha to mature TNFalpha. In the method, corporated of the proTNFalpha is measured by a colourimetric assay.

Che cleavage of the proTNFalpha is measured by a colourimetric assay.

Chis is then repeated in the presence of a test compound that is thought to inhibit this process. The results of the two reactions are then compared to determine whether the test compound is an inhibitor. The cleavage inhibitors can be used in the treatment of septic shock, rheumatoid arthritis, cachexia, cerebral malaria, ischaemia/reperfusion injury, graff-host disease, autoimmune diseases, and AIDS. PR-3 can be used to treat unwanted B cell/T cell interaction by contacting it with Sequence 256 AA;
                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PR-3; preproPR-3; MY17; human neutrophil protease-3; serine protease; tumour necrosis factor alpha; TNFalpha; H160; MY17; B cell; T cell; tumour necrosis factor alpha convertaes; cytokine; septic shock; rheumatoid arthritis; cachexia; cerebral malaria; graft-host disease; ischaemia/reperfusion injury; autoimmune disease; AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - useful for
                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "leader sequence present only in preproPR-3"
                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-MAR-1994; US-208574.

19-ARR-1994; US-230428.

27-FBE1995; US-395456.

(CETU ) CETUS ONCOLOGY CORP.

Halenback RF, Jewell DA, Koths KE, Kriegler M, Perez C;

WPI: 95-328287/42.

W-PSDB; T02265.
   Length 256;
                                                                           9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identification of inhibitors of mature INFalpha prodn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "dipeptide present in proPR-3"
   Score 64; DB 9; L
Pred. No. 9.25e+01;
                                                                       7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "mature PR-3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                              1 RPGPPGLQGRLQRLLQANGNHAAGIL 26
                                                                                                                                                  4 rppspalasvilalilsgaaraaeiv 29
                                                                                                                                                                                                                                                                                                                                                                     R85639 standard; Protein; 256 AA.
Query Match 31.8%;
Best Local Similarity 38.5%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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/note= "c
28..256
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02-MAR-1995; U02513
                                                                                                                                                                                                                                                                                                                                                                                                                                     23-APR-1996 (fi.
MY17 preproPR-3.
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Gaps

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9; Indels

Length 256;

Score 64; DB 15; Pred. No. 9.25e+01;

7; Mismatches

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production of tylosin-related polyketide compounds claim of tylosin-related polyketide compounds claim of tylosin-related polyketide compounds claim 9; Pages 103-109; 20pp; English.

Wizzol wizzoo represent proteins encoded by the tylactone synthase gene cluster of the invention. The gene cluster is also referred to as the tyla gene, and was isolated from Streptomyces fradiae. These sequences are multifunctional proteins which direct the synthesis of the polyketide tylactone, isolated from Streptomyces fradiae. Tylactone is the basic building block of the antibiotic tylosin. The DNA sequence can be modified so as to alter the type of carboxylic acids incorporated, the number of carboxylic acids incorporated and/or the post-condensation reactions performed, thereby resulting in novel tylosin-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 55; Fig 23; 91pp; English.

3 Polypeptide sequences (W19629-30 and W00918) can be deduced from the vep ORT in polyferide synthase (PKS) gene cluster (T68715) of Streptomyces venezuelae. The sequence data indicate that the PKS gene cluster encodes a polyene of 12 carbons. The vep gene cluster contains 5 PKS modules, plus a 5' loading module and a 3' end domain. Each of the sequenced modules includes a keto-ACP, an acyltransferase, a dehydratase, a keto-reductase and an acyl carrier protein domain. A novel expression cassette encoding the first module from the vep gene cluster and module 7 from the Streptomyces trylp gene cluster has polyhydroxyalkanoate (PHA) monomer synthase activity and can be used for PHA prodn. In host (esp. insect) cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Expression cassettes for production of polyhydroxyalkanoate(s) provide wide range of biodegradable polymers for medical or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W19629;
01-SEP-1997 (first entry)
Streptomyces venezuelae polyketide synthase.
Polyketide synthase; polyhydroxyalkanoate monomer synthase;
polyhydroxybutyrete; blodegradable polymer; vep gene;
metabolic engineering.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 63; DB 25; Length 1841; Pred. No. 1.11e+02;
                                                                                                      'note= "acyl carrier protein domain, ACP7"
                 /note= "acyltransferase domain, AT7"
1171..1355
/note= "ketoreductase domain, KR7"
1443..1526
                                                                                                                          1663..1695
/note= "thioesterase domain, TE7"
                                                                                                                                                                                                                                                                                 Sutton KL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Mismatches
                                                                                                                                                                                                                                                      (ELIL ) LILLY & CO ELI.
Dehoff BS, Kuhstoss SA, Rosteck PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1513 rdtpaalaahlaellatardhgpg 1536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for use as a biodegradable polymer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JT 14
W19629 standard; Protein; 4630 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Williams MD, Xue Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RPGPPGLOGRLORLLOANGNHAAG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Conservative
581..913
                                                                                                                                                                                                            19-FEB-1997; 301056.
22-FEB-1996; US-012078.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces venezuelae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-008847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-DEC-1995; US-008847 (MINU ) UNIV MINNESOTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-DEC-1996; U20119.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1841 AA;
                                                                                                                                                                                                                                                                                                 WPI; 97-418046/39.
N-PSDB; T80413.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sherman DH, Willia
WPI; 97-341701/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; T68715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               industrial use
                                                                                                                                                                    EP-791655-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polyketides
                                                                                                                                                                                               27-AUG-1997
                                                                                                                                                                                                                                                                                 Dehoff BS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                          Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W19629;
  Domain
                                                                                    Domain
                                                                                                                              Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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        Edysteroid dependent regulation of genes in mammalian cells -
for induced expression of heterologous genes
for induced expression of heterologous genes
bisclosure; F19 1, 45pp; English.
This sequence represents an ecdysteroid receptor DHR23alpha. DHR23-
alpha is a Drosophila steroid receptor homologue which can function as
a ligand-dependant transcription factor in mammalian cells when induced
by specific ecdysteroids such as DHR23alpha. The activity of DHR33-
alpha is induced upon administration of certain ecdysteroids but not
any of the mammalian hormones tested. DHR23alpha has been reported to
                                                                                                                                                                                                            regulate transcription of genes containing ecdysone response elements
in Drosophila tissue culture cells treated with 20-0H ecdysone.
                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tylactone synthase ORF5 protein.
Tylactone synthase gene cluster; tylg gene; multifunctional protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 benign inducing factors
Claim 24; Page 103; 126pp; English.
The amino acid sequence codes for the (20-OH) ecdysone receptor
protein which is part of the insect steroid receptor superfamily.
It can be used to screen for liquids specific for the insect
steroid receptors which can be used as highly specific and highly
active pesticides which are biodegradable. See also R13791-R13794.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding insect steroid receptors - and ligands, for use as
                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note- "zinc-finger DNA-binding domain C"
                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 878;
                                                                                                                                                                                                                                                                                                     Length 878;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 63; DB 3; Length 878; Pred. No. 1.11e+02; 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polyketide; tylactone synthesis; antibiotic; tylosin.
Streptomyces fradiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "hormone-binding domain E"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note- "ketosynthase domain, KS7
                                                                                                                                                                                                                                                                                                   Score 63; DB 6; L
Pred. No. 1.11e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ecdysone receptor.
Insect steroid receptor; EcR; hormone; DHR23.
                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
264.329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ze-FEB-1990; US-485749.
(STRD ) LELAND STANFORD JR UNIV.
Hogness DS, Koelle MR, Segraves WA;
WPI; 91-281480/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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W22605 standard; Protein; 1841 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T 12
R13793 standard; Protein; 878 AA.
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larity 64.3%;
Conservative
                                                                                                                                                                                                                                                                                                 31.3%;
Similarity 64.3%;
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-NOV-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-FEB-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              431..651
/note= "h
                                                                                                                                                                                                                                                                                                                                                                                         738 ppqlqgqlqpqlqp 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                               4 PPGLOGRLORLLOA 17
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                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-SEP-1991.
15-FEB-1991; U01189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      878 AA;
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                                                                                                                                                                                                                                                           Sequence
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R13793;

RESULT

Matches

셤

domain domain

CCCSTTRANGARDACC

Domain

Key

Matches

셤 ö RESULT

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Gaps

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8; Indels

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Novel human type alpha-1 (XVIII) collagen is characterised by triple helical domains containing the GXXGX'Y' motif (where X, Y, X' and Y' represent any amino acid), the helical domains being separated and flanked by non-triple helical regions which may provide flexibility. Alpha-1 collagen is expressed in multiple provide flexibility. Alpha-1 collagen is expressed in multiple comprising alpha-1 collagen nucleic acid (see T84484) and an expression control sequence can be used to express recombinant collagen in prokaryotic or eukaryotic (especially mammalian) host cells. The alpha-1 collagen may be used to treat a patient suffering from a disease associated with cartilage degradation, and for supplementing collagen. It can also be used as a connective tissue filler (e.g. for plastic surgery), can be interposed between a dermal equivalent and skin to improve adhesion, and as a substract on which to grow epithelium. The addition of glycosaminoglycans makes alpha-1 collagen a better carrier for fibroblast growth factor, and imparts greater tensile strength.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid encoding human alpha-1 collagen - for production of recombinant alpha-1 collagen, for use in the treatment of cartilage
                                      329..334
/label= GXYGX'Y'_motif
/note= "Claim 1"
                                                                                                                   335..340
/label= GXYGX'Y'_motif
/note= "Claim 1"
                                                                                                                                                                                                                                                                         1abel - GXYGX'Y'_motif
note - "Claim 1"
                                                                                                                                                                                                                                                                                                                                                                                                                      523..528
/label= GXYGX'Y'_motif
/note= "Claim 1"
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/label= GXYGX'Y'_motif
/note= "Claim 1"
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/label= GXYGX'Y'_motif
/note= "Claim 1"
/label= GXYGX'Y'_motif
/note= "Claim 1"
                                                                                                                                                                                           354..359
/label= GXYGX'Y'_motif
/note= "Claim 1"
                                                                                                                                                                                                                                                                                                                                                                        /label= GXYGX'Y'_motif
/note= "Claim 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUL-1997.

01-DEC-1993; 159784.

01-DEC-1993; US-159784.

(HARD) HARVARD COLLEGE.

Oh SP, Olsen BR;

WPI; 97-350247/32.
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                                                                                                                   peptide
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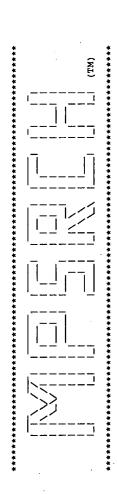
ö Score 62; DB 24; Length 684; Pred. No. 1.34e+02; 1; Indels 0; Mismatches Query Match
Best Local Similarity 88.9%;
Matches 8; Conservative

213 rpgppglpg 221 윱 ò

1 RPGPPGLQG 9

Search completed: Thu Jul 30 09:33:56 1998 Job time: 20 secs.

US-08-938-548A-12.rai



Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu Jul 30 09:36:05 1998; MasPar time 1.18 Seconds 138.599 Million cell updates/sec :uo

>US-08-938-548A-12 (1-28) from US08938548A.pep 201 rbular output not generated.

1 RPGPPGLQGRLQRLLQANGNHAAGILTM 28 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

Post-processing: Minimum Match 0% Listing first 45 summaries

63816 seqs, 5850866 residues

Searched:

a-issued 1:5_COMB 2:PCT9_COMB 3:backfiles Database:

Mean 20.372; Variance 82.258; scale 0.248 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	o 2.07e+01	.o 2.50e+01	i 2.50e+01	.o 4.40e+01	o 6.39e+01						:1 6.39e+01			i 6.39e+01			:i 6.39e+01		:i 6.39e+01	.o 7.69e+01	:i 9.24e+01	:1 9.24e+01	:1 9.24e+01
	Applicatio	Applicatio	, Applicati	Applicatio	Applicatio	Applicatio	Applicatio	Applicatio	Applicatio	Applicatio	, Applicat	Applicatio	, Applicati	, Applicati	Applicatio	Applicatio	, Applicati	, Applicati	, Applicati	Applicatio	, Applicati	, Applicat	, Applicati
ion	, ,	4	10	7	'n	œ	'n	'n	4	4	14	4	14	14	4	4	14	74	14	ý	25	10	43
Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence					-		Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
A	PCT-US91-0	PCT-US95-1	US-08-469-	US-08-494-	US-08-115-	US-08-792-	US-07-941-	PCT-US93-0	US-07-949-	US-08-017-	US-07-745-	US-08-115-	US-08-165-	US-07-921-	US-07-941-	PCT-US93-0	PCT-US94-1	ns-07-688-	PCT-US91-0	PCT-US96-1	ns-01-176-	US-07-924-	US-08-062-
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Length	10	716	2509	1694	199	199	199	199	199	199	296	296	296	296	296	296	296	405	405	176	26	27	27
% Query Match	32.8	32.3	32.3	30.8	29.9	29.9	29.9	29.9	29.9	29.9	29.9	29.9	29.9	29.9	29.9	29.9	29.9	29.9	29.9	29.4	28.9	28.9	28.9
Score	99	65	65	62	9	9	09	9	9	9	9	09	9	9							28	28	28
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No. 5215895. No. 5215895. No. 5215895. No. 2, Application of 2549860. No. 517555. No. 54, Application of App	AA.	sion #1.25
Patent N Patent N Sequence Patent N Patent N Patent N Patent N Patent Sequence Seque	. 10	H H
5215895-4 5215895-3 US-08-07-949- US-08-017- 549860-017- 517525-8 517525-8 517525-8 517525-8 0S-08-186- US-08-186- US-08-186- US-08-186- US-08-08-186- US-07-946- US-07-946- US-07-946- US-07-946- US-07-946- US-07-97-	PR' PR' 9104588	COMP COMP 29th MS-DO MS-DO MS-10 S91/0 /544,
	PC PC	wwing, Jeffre- carl F. TION: SURFAC SNCES: 3 ADDRESS: 8 ADDRESS: 8 Third Avenue Trk Tork Tork Tork Tork Tork Tork Tork
199 199 199 199 241 241 282 1367 1367 1367 1367 1367 1367 1367 1367	88-3 ST Application Applicatio	NWT: Browning, Jeffrey NWT: Ware, Carl F. PENVENTION: SURFACE OF SEQUENCES: 3 SSSEE: C/O Fitsh & Neav. STE 875 Third Avenue, THE 875 Third Avenue, THE 875 Third Avenue, THE 875 THIRD AVENUE, TOWN YORK TYPE: FLOPPY disk TYPE: POTONING SYSTEM: PCT/US TYPE: PAPLICATION DATA: TREALON NUMBER: PCT/US TREALON NUMBER: US 07/ THE 12 12-715-0600 THE 14-8367 TON FOR SEQ ID NO: 3: THE 10 amino acids TAMINO ACID TON FOR THE AMINO ACID
0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,	4588-: , App. 3, Apl	APPLICANT: Browning, Jeffre APPLICANT: Ware, Carl F. TITLE OF INVENTION: SURPACE NUMBER OF SEQUENCES: 3 CORRESSPONDERSES: Nea STREET: 875 Third Avenue, CITY: New York COUNTRY: USA COUNTRY: USA COUNTRY: USA COUNTRY: USA COUNTRY: LEMP COMPATER: MEDION TYPE: Floppy disk COUNTRY: DAP COUNTRY: DAM COUNTRY COUNTRY: DAM COUNTRY CO
	1 -US91 xxx uence quenc	APPLICANT TITLE OF NUMBER OF CORRESPON ADDRESS'S STREET: CITY: STATE: STATE: COMPUTER MEDIUM COMPUTER MEDIUM COMPUTER MEDIUM APPLICAM FILING FILING ATTORNEY NAME: REGISTR REG
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	SULT	88888888888888888888888888888888888888

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Sequence 8, Application US/08792019B
Patent No. 5741772
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: 1840 DEHAVILLAND DRIVE
CITY: THOUSAND OAKS
STRATE: CAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 60; DB 1; Length 199;
Pred. No. 6.39e+01;
3; Mismatches 0; Indels
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, P.O. Box 457
CITY: Spring House
STRIE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792,019B
FILING DATE: 03-FEB-1997
                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/115,680
                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/941,372
FILING DATE: 02-SEP-1992
ATTORNEY/ACENT INFORMATION:
NAME: Bak, MATY E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: INDIAUSA
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-9206
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 199 annino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
JENCE 199 AA; 21429 MW; 188641 CN;
                                                                                                                    ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/08792019B
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 29.9%;
Best Local Similarity 70.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
GY: linear
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US-08-792-019B-8
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                                                                                              Sequence 2, Application US/08494168
Patent No. 5731192
APPLICANT: Reders, Stephen T. APPLICANT: Edou, Jing TITLE OF INVENTION: Collagen COL4A6: Gene, Protein and Method TITLE OF INVENTION: Of Detecting Collagen Deficiency NUMBER OF SEQUENCES: 10
CORRESPONDENCES. 10
CORRESPONDENCE ADDRESS: ADDRESSE: Foley, & Lardner STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Patent No. 5437863
GENERAL INFORMATION:
APPLICANT: Williams, David A.
APPLICANT: Clark, Steven C.
TITLE OF INVENTION: Method of Treating Cell Damage or
TITLE OF INVENTION: Depletion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 62; DB 1; Length lost
Pred. No. 4.40e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                     COPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DAYA:
APPLICATION NUMBER: US/08/494,168
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/112,465
PILING DATE: 27-AUG-1993
ATTONEY/AGENT INFORMATION:
NAME: SAXE, Bernhard O:
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 28,665
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          199 AA.
                                                                                                                                                                                                                                                                                    ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
JENCE 1694 AA; 165283 MW; 14956750 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 20007-2109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRD FC COMPATIBLE
COMPUTER: IRD FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-D
SOFTWARE: PatentIn Release #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08115680
                                                               Sequence 2, Application US/08494168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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Sst Local Similarity 88.3°,
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Clark, St. TITLE OF INVENTION: 1 TITLE OF INVENTION: 1 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
GY: linear
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RESULT

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Gaps

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Sequence 14, Application US/07745382
Patent No. 5270181
GENERAL INFORMATION:
APPLICANT: MCCOY, John
APPLICANT: LaVallie, Edward
TITLE OF INVENTION: Peptide and Protein Fusions To
TITLE OF INVENTION: Thioredoxin and Thioredoxin-Like Molecules
NUMBER OF SEQUENCES: 24
CORRESPONDENCE 20
ADDRESSE: Genetics Institute, Inc.
STREET: MASSACHUSETES
COUNTRY: U.S.A.
ZIP: O2140
COMPUTER READABLE FORM:
MEDIUM TYPE: IDPPPY disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
GURBENT APPLICATION DATA: 125
FILING DATE: 19910814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                       CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/017,522A

FILING DATE: 19930212

CLASSIFICATION: 530

ATTONREY/AGENT INFORMATION:

NAME: WELNERT, M C

REGISTRATION NUMBER: 31,544

REFERENCE/POCKET NUMBER: 31,544

REFERENCE/POCKET NUMBER: 31,544

REFERENCE/POCKET NUMBER: 31,544

REFERENCE/POCKET NUMBER: 31,544

RELEPRATION INFORMATION:

TELEPOMMUNICATION INFORMATION:

TELEPOMMUNICATION INFORMATION:

TELEPOMMUNICATION ON: 4:

SEQUENCE CHRARACTERISTICS:

LENGTH: 199 amino acids

TENGTH: 199 amino acids

TYPE: AMINO ACID

STRANDENESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 60; DB 1; Length 199;
Pred. No. 6.39e+01;
3; Mismatches 0; Indels
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/652,531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
SEQUENCE 199 AA; 21429 MW; 188641 CN;
                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/07745382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 29.9%;
Best Local Similarity 70.0%;
Matches 7; Conservative
                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
       CAMBRIDGE
MA
       129 LQARLDRLLR 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 LOGRIORLIO 16
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US-07-745-382-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                          CUNTRY: USA

STATE: WA

COUNTRY: USA

ZIPE: 02140

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CC CURSTICATION NUMBER: US/07/949,516A
CC FILING DATE: 19-NOV-1992
CC ATTONEY/AGENT INFORMATION:
CC ATTONEY/AGENT INFORMATION:
CC REGISTRATION NUMBER: 31,544
CC REGISTRATION OF 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 199 amino acids
"VPE: amino acid
"VPE: amino acid
"VPE: amino acid
"VPE: with 199 amino acid
"VPE: amino acid
"VPE: with 199 amino acids
"VPE: amino acid
"VPE: with 199 amino acids
"VPE: with 198641 CN;
"VPE: WITH 199 amino acids
"V
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STREET: 87 CAMBRIDGEPARK DRIVE
                                                                                                                                                                                                      Sequence 4, Application US/07949516A
Patent No. 5700664
GENERAL INFORMATION:
APPLICANT: Tanney V.-Chung
APPLICANT: Bennett, Frances
TITLE OF INVENTION: A MAMMALIAN CYTOKINE, IL-11
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LEGAL AFFAIRS
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MAMMALIAN CYTOKINE, IL-11
CORRESPONDENCE ADDRESS:
ADDRESSEE: LEGAL AFFAIRS
STREET: ST. Cambridge
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08017522A
Patent No. 5371193
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
PAUL, STEPHAN R
APPLICANT: PAUL, STEPHAN R
APPLICANT: YANG, YU-CHUNG
TITLE OF INVENTION: A MAMMALIAN CYTOKINE, IL-11
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LEGAL AFFAIRS - GENETICS INSTITUTE, II
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                             PRT;
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                                                                                                                                                                        Sequence 4, Application US/07949516A
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70.0%;
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Best Local Similarity
Matches 7; Conserv
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7 LQGRLQRLLQ 16
JT 10
US-08-017-522A-4
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Search completed: Thu Jul 30 09:36:12 1998 Job time: 7 secs.
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                                                                                               Sequence 14, Application US/07921848
Patent No. 5292646
GENERAL INFORMATION:
APPLICANT: MCCOY, John
APPLICANT: LaVallie, Edward
TITLE OF INVENTION: Peptide and Protein Fusions To
TITLE OF INVENTION: Thioredoxin and Thioredoxin-Like Molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Pred. No. 6.39e+01;
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/921,848
FILING DATE: 19920728
  296 AA
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/652,531
FILING DATE: 06-FEB-1991
PRIOR APPLICATION NUMBER: US 07/745,382
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                           E: Genetics Institute, Inc.
87 CambridgePark Drive
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: CSerr, Luann
REGISTRATION NUMBER: 31,822
REGISTRATION NUMBER: G15188A
TREECCMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
JENCE 296 AA; 31769 MW; 414378 CN;
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                                                                                                                                                                                                                      STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
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                                                                          Sequence 14, Application US/07921848
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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AMINO ACID
 STANDARD;
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                                                                                                                                                                                     NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
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70.0%;
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Matches 7; Conserv
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US-07-921-848-14
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US-07-941-372-4
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GENERAL INFORMATION:
APPLICANT: Williams, David A.
APPLICANT: Clark, Steven C.
TITLE OF INVENTION: Method of Treating Cell Damage or TITLE OF INVENTION: Depletion
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Center, P.O. Box 457
CITY: Spring House
STATE: Pennsylvania
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Pred. No. 6.39e+01;
....a+rhes 0; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/941,372
FILING DATE: 19920902
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/POCKET NUMBER: INDUSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
FENCE 296 AA; 31769 MW; 414378 CN;
                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (215) 540-9206
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 296 amino acids
TYPE: AMINO ACID
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29.9%;
Similarity 70.0%;
7; Conservative
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Best Local Similarity
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp uo un

Thu Jul 30 09:34:14 1998; MasPar time 4.39 Seconds 233.145 Million cell updates/sec

ular output not generated.

>US-08-938-548A-12 (1-28) from US08938548A.pep 201 1 RPGPPGLQGRLQARLOANGNHAAGILTM 28 Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

120441 seqs, 36531193 residues Searched:

Minimum Match 0% Listing first 45 summarles Post-processing:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d Database:

Mean 30.142; Variance 55.308; scale 0.545 Statistics:

Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Pred. No.	2.25e+00	2.25e+00	6.08e+00	6.08e+00	6.08e+00	8.42e+00	8.42e+00	8.42e+00	8.42e+00	8.42e+00	8.42e+00	8.42e+00	1.16e+01	1.16e+01	1.16e+01	1.60e+01	1.60e+01	2.20e+01	2.20e+01	2.20e+01	2.20e+01	2.20e+01	2.20e+01
	Description	superoxide dismutase	superoxide dismutase	mALDP protein - mouse	hypothetical protein		hypothetical protein	₽	transcription initiat	transcription initiat	transcription initiat	transcription initiat	PAS1 protein - yeast	deoxyuridine 5-tripho	hypothetical protein		adenylate cyclase (EC	fatty-acid synthase (hypothetical protein	proteinase 3 (EC 3.4.	hypothetical protein		protein-tyrosine-phos	protein-tyrosine-phos
	A	A41654	B41654	S47044	H64888	S23647	E69913	JH0496	S11712	S41307	JN0443	JN0445	A55152	D69081	S49183	S19248	A33988	G01880	S25618	PRHU3	S51155	S61858	A46101	B46101
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,	Length	187	187	736	879	2115	178	442	442	510	525	528	1157	150	253	319	1692	2509	239	256	263	439	535	548
dР	Query	35.3	35.3	33.8	33.8	33.8	33.3	33.3	33.3	33.3	33.3	33.3	33.3			32.8	32.3	32.3	31.8	31.8	31.8	31.8	٠	31.8
	Score	7.1	71	99	68	89	29	29	29	67	67	67	67	99	99	99	65	9	64	. 64	64	64	64	64
	Result No.	-	7	m	4	ស	φ	7	80	0	10	11	12	13	14	15	16	17	18	19	20	21	22	. 23

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sulfite reductase (fe probable epidermal ce	probable epideimai ce Yorl protein - yeast	hypothetical protein	ribosomal protein S2, hypothetical protein		hypothetical protein	collagen COLF1 - fres	ecdysone receptor - f	allergen TBA-1 - Toxo	calcium-binding prote	hypothetical protein	hypothetical protein	factor VIII-associate	hypothetical protein	collagen alpha 1(XVII			collagen alpha 6(IV)	collagen alpha 2(IV)
RDYCS7 A43917	S64616	\$12255	A42115 B64939	C64835	S77523	S31521	A41055	B49139	S26481	Q3YCRQ	S76765	A42832	876929	A53019	A45748	CGHUIB	CGHU6B	S16366
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9 4 4	64	63	63	63	63	63	63	62	62	62	62	62	62	62	62	62	62	62
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ALIGNMENTS

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		superoxide dismutase (EC 1.15.1.1) (Cu-Zn) precursor			12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change				×.		emophi]							48882	(u2		#length 187 #molecular-weight 19536 #checksum 584	Score 71; DB 2; Length 187;	Indele	2100				
		(Cu		ae	-Jung-				ds, B	7	oŧ							1D:91	(Cu-1		236	Leng		ò				
		15.1.1	į	#formal_name Haemophilus influenzae	ion 12				Kroll, J.S.; Langford, P.R.; Loynds, B.M.	49-745	Copper-zinc superoxide dismutase of	and Haemophilus parainfluenzae.						##cross-references GB:M84012; NID:g148881; PID:g148882	#superfamily superoxide dismutase (Cu-Zn)	ase	ght 19	DB 2;	7. 25e+0	20110				
	lete	(BC 1.	zae	lus ir	_revis				, P.R.	173:74	e dism	ainflu					o.	D:9148	de dis	reduct	ar-wei	71;	Pred. NO. 2.25e-	THETT	26	28		
	#type complete	utase	urrnen	emophi	dnence				ngford	1991)	eroxid	us par	55		λ		bel KF	12; NI	peroxi	oxido	olecul	Score	Pred.	,	VGTVTI	AGILTN		
	#typ	e dism	Haemopullus Iniluenzae	ame Ha	92 #se	1998			S.; La	iol. (nc sup	mophil	920416		preliminary		1-187 ##label KRO	B:M840	ily su	metalloprotein; oxidoreductase	87 #II	5.38;	7.74;) }	29 KPAGPSIEVKVQQLDPANGNKDVGTVTI 56	RPGPPGLQGRLQRLLQANGNHAAGILTM 28		
	554	eroxid	aemopn	mal_n	Jun-19	20-Mar-1998	554	554	11, J.	3acter	per-zi	d Hae	MUID:	554	prel	DNA	1-18	ces G	perfam	llopr	ngth 1		lty 3	1001	700LDP	CORLLO		
	A41654	dns	Ĭ,	#	12-	ñ	A41654	A41654	Kro		Cop	ď	sences	A41654		e_type	S	efere	#sn]	met	#]el		Similarity 35./*	3	SIEVK	GLOGR		
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ULT	RY	LE		ORGANISM	ы		ACCESSIONS	REFERENCE	#authors	#journal	#title		#cross	#accession	S##	E##	¥##	##	CLASSIFICATION	KEYWORDS	SUMMARY	uery M	Metchos	בכווכים	53	Н		
RESULT	ENTRY	TITLE		ORG	DATE		ACC	REF											CLA	KEY	SUM	O f	η >	4	g	ŏ	ı	

B41654 #type complete superoxide dismutase (EC 1.15.1.1) (Cu-2n) precursor -	Haemophilus paralifluenzae #formal_name Haemophilus parainfluenzae 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 20-Mar-1998	ESSIONS B41654 ESEMBRE A41654 #authors A41654 #journal J. Bacteriol. (1991) 173:7449-7457 #title Copper-zinc superoxide dismutase of Haemophilus influenzae #cross-references MUID:92041655 #accession B41654
RESULT 2 ENTRY TITLE	ORGANISM DATE	ACCESSIONS REFERENCE # authors # journal # title #cross-refere

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7 LQGRLQRLLQANGNHAAGILTM 28
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#description
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Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror, S.J.; Serror, P.; Shin, B.S.; Soldo, B.; Sorokin, A.; Tacconi, E.; Takagi, T.; Takahashi, H.; Takemaru, K.; Takeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, S.; Vandenbol, M.; Vannier, F.; Vassarotti, A.; Vanti, A.; Wambutt, R.; Wedler, E.; Wedler, H.; Weltzenegger, T.; Winters, P.; Wipat, A.; Yasanoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Yoshikawa, H.; Zumsteln, E.; Yoshikawa, H.; Danchin, A. Nature (1997) 390:249-256

The complete genome sequence of the Gram-positive bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JH0496 #type complete transcription initiation factor sigma homolog - Streptomyces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #authors Shiina, T.; Tanaka, K.; Takahashi, H.
#journal Gene (1991) 107:145-148
#title Sequence of hrdB, an essential gene encoding sigma-like
transcription factor of Streptomyces coelicolor A3(2):
homology to principal sigma factors.
#cross-references WUID:92077425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *superfamily transcription initiation factor sigma katF; transcription initiation factor sigma katF homology DNA binding; sigma factor; transcription initiation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sigma-like transcription factor
#formal_name Streptomyces coelicolor
31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change
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#length 442 #molecular-weight 48364 #checksum 4785
                                                                                                                                                                                                                                                                                                                                                                                                                                             yonC
#length 178 #molecular-weight 19609 #checksum 8831
                                                                                                                                                                                                                                                                                                          preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                        ##residues 1-178 ##label KUN
##experimental_source strain 168
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##residues 1-442 ##label SHI
##cross-references EMBL:X52983
                                                                                                                                                                                                                                                                    Bacillus subtilis.
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LQGRLQRLLQANGNHAAGIL 26
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JH0496
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Matches 9; Conser
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Matches 7; Conser
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JH0496
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#gene
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ENTRY
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Velasco, J.; Martin, J.F. submitted to the EMBL Data Library, December 1993 Organization and expression of the hrdB-sprC gene cluster of streptomyces griseus encoding a sigma factor protein and a serine protease. Role on growth and sporulation of
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66-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
08-Sep-1997
$41307
Marcos, A.T.; Diez, B.; Gutierrez, S.; Fernandez, F.J.;
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    Streptomyces

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transcription initiation factor sigma katF homology
DNA binding; sigma factor; transcription initiation
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transcription initiation factor sigma katF homology
DNA binding; sigma factor; transcription initiation
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homology #label KTF
#length 442 #molecular-weight 48413 #checksum 4794
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                                                                    #formal_name Streptomyces coelicolor
03-May-1994 #sequence_revision 20-Feb-1995 #text_change
06-Sep-1997
S11712
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#length 510 #molecular-weight 55795 #checksum 1415
                                                                                                                                                                                             Tanaka, K.; Shiina, T.; Takahashi, H.
submitted to the EMBL Data Library, May 1990
Multiple homolog genes for principal sigma subunit
Streptomyces coelicolor A3(2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 442;
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                                                                                                                                                                                                                                                                                                                                                              ##cross-references EMBL:X52983; NID:g48744; PID:g48745
##experimental_source strain A3(2)
Score 67; DB 2; LA
Pred. No. 8.42e+00;
11; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                            1-442 ##label EMB
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##residues
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Similarity 31.8%;
7; Conservative
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Best Local Similarity 31.8%;
Matches 7; Conservative
                                               coelicolor
                                                                                                                                                                                                                                                                                                                   ##molecule_type DNA
##residues 1-44
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Matches
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Oguiza, J.A.; Martin, J.F.
submitted to the EMBL Data Library, June 1994
Three genes hrdb, Thand and hrdf of Streptomyces griseus IMRU
3570, encoding sigma factor-like proteins, are
differentially expressed under specific nutritional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 replacing a palindromic 34bp intergenic sequence.
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RNA-directed DNA polymerase (EC 2.7.7.49), msDNA specific
Escherichia coli retron Ec107
DNA nucleotidyltransferase (RNA-directed); reverse
                                                                                                                                                                                                                                                                                  849183 #type complete
hypothetical protein - Streptomyces griseus
#formal_name Streptomyces griseus
16-Feb-1995 #sequence_revision 12-May-1995 #text_change
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#formal_name Escherichia coli retron Ec107
20-Feb-1995 #sequence_revision 15-Oct-1996 #text_change
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                  MTH1605
#length 150 #molecular-weight 16996 #checksum 5013
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                                                                     Score 66; DB 2; Densor.
Pred. No. 1.16e+01;
....matches 4; Indels
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Pred. No. 1.16e+01;
5; Mismatches 10; Indels
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##cross-references EMBL:X62583; NID:g42774; PID:g42775
##experimental_source E. coll wild strain
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Retron Ec107 is inserted into the Es
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##molecule_type DNA
##residues 1-253 ##labe
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                                                                             32.8%;
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Best Local Similarity 37.5%;
Matches 9; Conservative
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                                                                                                                       Conservative
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S49183
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##molecule_type DNA
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Best Local Similarity
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#authors
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DATE
                    #gene
SUMMARY
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GENETICS
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Best Local Similarity 50.0%; Pred. No. 1.16e+01;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps
Db 287 ALGGRINWILQINPEDEA 304
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Search completed: Thu Jul 30 09:34:34 1998 Job time: 20 secs.

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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu Jul 30 09:34:53 1998; MasPar time 2.66 Seconds 263.713 Million cell updates/sec hlar output not generated. Run on:

>US-08-938-548A-12 (1-28) from US08938548A.pep 201 Description: Perfect Score: Sequence: Title:

1 RPGPPGLQGRLQRLLQANGNHAAGILTM 28

PAM 150 Gap 15 Scoring table:

Searched:

69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

swiss-prot35 1:swiss1

Mean 31.553; Variance 48.558; scale 0.650 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Score	% Query Match	Length DB	DB	£	Description	Pred. No.
2.0		101	-	Adaka Daca	d governor of governor	
3.0		187	-	SODO HARTN		5.60e-01
34.3		1992	ı ~	TR12 HUMAN	THYROID RECEPTOR INTER	1,20e+00
33.8		736		ALD MOUSE	ADRENOLEUKODYSTROPHY P	1.74e+00
33.8		879	Н	YDBH_ECOLI	HYPOTHETICAL 96.8 KD P	1.74e+00
33.3		79	Н	NIFU_FRAAL	NIFU PROTEIN.	2.53e+00
33.3		442	Н	HRDB_STRCO	RNA POLYMERASE PRINCIP	2.53e+00
33.3		1157	-	PEX1_PICPA	PEROXISOME BIOSYNTHESI	2.53e+00
32.8		398	Н	VE2_HPV63	REGULATORY PROTEIN E2.	3.65e+00
32.3		307	Н	CC36_CAEEL	CUTICLE COLLAGEN 36.	5.25e+00
32.3		368	Н	COA1_POVLY	COAT PROTEIN VP1.	5.25e+00
32.3		799	М	AFSK_STRCO	SERINE/THREONINE PROTE	5.25e+00
32.3		1692		CYAA_SCHPO	ADENYLATE CYCLASE (EC	5.25e+00
31.8		199	~1	IL11_MOUSE	INTERLEUKIN-11 PRECURS	7.52e+00
31.8		256	Н	PRN3_HUMAN	MYELOBLASTIN PRECURSOR	7.52e+00
31.8		624	Н	SIR_SYNP7	SULFITE REDUCTASE (FER	7.52e+00
31.8		1477	Н	YOR1_YEAST	OLIGOMYCIN RESISTANCE	7.52e+00
31.3		255	П	YPE1_RHORU	HYPOTHETICAL 28 KD PRO	1.07e+01
31.3		394	Н	RT04_YEAST	MITOCHONDRIAL 40S RIBO	1.07e+01
31.3		702	-	YCBY_ECOLI	HYPOTHETICAL 78.9 KD P	1.07e+01
31.3		878	Н	ECR_DROME	ECDYSONE RECEPTOR (ECD	1.07e+01
30.8		256	Н	YREC_SYNP2	HYPOTHETICAL 28.7 KD P	1.52e+01
30.8		380	Н	F812_MOUSE	FACTOR VIII INTRON 22	1.52e+01

1 530+01	10792C.1	1.52e+01	1.52e + 01	1.52e + 01	1.52e+01	1.52e+01	1.52e+01	2.15e+01	2.15e+01	2.15e+01	2.15e+01	2.15e+01	2.15e+01	2.15e+01	2.15e+01	2.15e+01	2.15e+01	2.15e+01	2.15e+01	3.03e+01	3.03e+01	3.03e+01
ENAS GEVENTOOMS ON THE OCK	4	RNA POLYMERASE SIGMA F	COLLAGEN ALPHA 1(XVIII	COLLAGEN ALPHA 6(IV) C	COLLAGEN ALPHA 4(IV) C	COLLAGEN ALPHA 2(IV) C	PROCOLLAGEN ALPHA 2(IV	HYPOTHETICAL PROTEIN M	NEGATIVE FACTOR (F-PRO	TRANSCRIPTIONAL REGULA	HYPOTHETICAL OXIDOREDU	PULMONARY SURFACTANT-A	BETA-ARRESTIN 2.	BETA-ARRESTIN 2 (ARRES	PROTEIN UL88.	REGULATORY PROTEIN E2.	LEGUMIN PRECURSOR (BET	PHEROMONE B ALPHA 2 RE	PROBABLE DNA PACKAGING	THERMOSTABLE CARBOXYPE	COENZYME POO SYNTHESIS	COLLAGEN ALPHA 1(XI) C
CONTO CONTO	ASSI_SINIS	RPSD_CAUCR	CA1H_HUMAN	CA64_HUMAN	CA44_HUMAN	CA24_CAEEL	CA24_ASCSU	Y652_METJA	NEF_HV2NZ	BASR_SALTY	YDGB_ECOLI	PSPA_HUMAN	ARR2_HUMAN	ARR2_BOVIN	UL88_HCMVA	VE2_HPV09	LEG1_GOSHI	BAR2_SCHCO	VTER_EBV	CTAQ_THEAQ	POOF_PSEFL	CAIB MOUSE
-	4	-	Н	Н	Н	-	~	-	Н	Н	Н	г	Н	Н	Н	Н	Н	Н	-	Н	Н	7
0	004	652	684	1678	1690	1758	1763	134	180	222	240	248	409	420	429	461	516	518	069	511	829	1804
0	20.0	30.8	30.8	30.8	30.8	30.8	30.8	30.3	30.3	30.3	30.3	30.3	30.3	30.3	30.3	30.3	30.3	30.3	30.3	29.9	29.9	29.9
Ç	70	62	62	62	62	62	62	61	61	61	61	61	61	61	61	61	61	61	61	9	9	9
7.	+7	52	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Query Match 35.3%; Score 71; DB 1; Length 187; Best Local Similarity 35.7%; Pred. No. 5.60e-01;

Gaps

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3; Indels Length 79;

Best Loc Matches

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-!- FUNCTION: THE SIGMA PACTOR IS AN INITIATION FACTOR THAT PROMOTES ATTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES AND THEN IS RELEASED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGMA-54 FAMILY.

EMBL; X52083; 648745; -.

PIR; X1712; S11712; S11712; S16470_1; 1.

PROSITE; PS00716; SIGMA70_2; 1.

TRANSCRIPTION REGULATION; SIGMA FACTOR; DNA-DIRECTED RNA POLYMERASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POLYMERASE CORE BINDING (POTENTIAL).
H-T-H MOTIF (BY SIMILARITY).
4720321F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: TO OTHER SIGMA FACTORS THAT DO NOT BELONG TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; STREPTOMYCETACEAE.
     PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; FRANKIACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEX1_SICPA STANDARD; PRT; 1157 AA. P46463; 01-NOV-1995 (REL. 32, CREATED) 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE) 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE) PRENXISOME BIOSYNTHESIS PROTEIN PASI (PEROXIN-1). PEXI OR PASI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                Score 67; DB 1; L
Pred. No. 2.53e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 67; DB 1; I
Pred. No. 2.53e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1990 (REL: 16, CREATED)
01-NOV-1990 (REL: 16, LAST SEQUENCE UPDATE)
01-NOV-1992 (REL: 23, LAST ANNOTATION UPDATE)
RNA POLYMERASE PRINCIPAL SIGMA FACTOR HRDB.
                                                                                                                                                                                                                                                          4CF1624F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 442 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
                                                                                   STRAIN-CPII;
MEDLINE: 95369734.
HARRIOTT O.T., HOSTED T.J., BENSON D.R.
GENE 161:65-67(1995).
EMBL: 129299; 6497438; -.
NITROGEN FIXATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMAIN=43(2);
MEDLINE; 89058616.
TANNKA K., SHIINA T., TAKAHASHI H.;
SCIENCE 242:1040-1042(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    370 LQEQLHSVLDTLSEREAGVVSM 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | | :|: :|: ::: ||:::|
7 LQGRLQRLLQANGNHAAGILTM 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48413 MW;
                                                                                                                                                                                                                                           XATION.
79 AA; 8624 MW;
                                                                                                                                                                                                                                                                                                                33.3%;
larity 56.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 31.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             | |:|::||:||||
| RPGPPGLQGRLQRLLQ 16
                                                                                                                                                                                                                                                                                                                                                                                                                             29 RRGAPAPDRRLRRLLQ 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREPTOMYCES COELICOLOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PICHIA PASTORIS (YEAST)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246
422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            233 2
403 4
442 AA;
                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HRDB_STRCO
P18183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA-BINDING
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SEQUENCE
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     SWARKARO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
BLATINER F.R., PLUNKETT G. III, MAXHEW G.F., PERNA N.T., GLASNER F.D.;
SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AIBA H., BABA T., FUJITA K., HAYASHI K., HONJO A., HORIUCHI T., ITEMOTO K., ITADA T., ISONO K., ISONO S., ITOH T., KANAI K., KASAI H., KASHIMOTO K., KIM S., KIMMEA S., KITAGAMA M., KITAKAWA M., MAKINO K., MASUDA S., MIKI T., MIZOBUCHI K., MORI H., MOTOMURA K., NAKAMURA Y., NASHIMOTO H., NISHIO Y., OSHIMA T., SAITO N., SAMPEI G., SEKI Y., TAGAMI H., TAKRMOTO K., WADA C., YAMAMOTO Y., YANO M.; SUBEL Y., SALTO K., WADA C., YAMAMOTO Y., YANO M.; SUBEL Y., SUBMITTED (DEC-1996) TO EMBL/GENDANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ESCHERICHIA COLI.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC
ENTEROBACTERIACEAE.
                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                 P52645; P77502; P76855; 01-0CT-1996 (REL. 34, CREATED) 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE) 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE) HYPOTHETICAL 96.8 KD PROTEIN IN LDHA-TYNA INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BUNCH P.K., MAT-JAN F., LEE N.A., DEAYALA B.A., CLARK D.P.; SUBMITTED (NOV-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                      Score 68; DB 1; Length 736;
Pred. No. 1.74e+00;
5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 33.8%; Score 68; DB 1; Length 879; Best Local Similarity 45.8%; Pred. No. 1.74e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 36 I -> L (IN REF. 3).
879 AA; 96834 MW; 8BFD7CF3 CRC32;
  81858 MW; D373B00E CRC32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32, CREATED)
32, LAST SEQUENCE UPDATE)
34, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                             879 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79 AA
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                                                                                                                                                                      704 AGIPKMOGRLQELRQILGEAAAPVQPL 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RUDD K.E.;
UNPUBLISHED OBSERVATIONS (MAR-1996).
                                                                                                                                                                                                         2 PGPPGLQGRLQRLLQANGNHAAGILTM 28
                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U36928; -; NOT_ANNOTATED_CDS.
ECOGENE; EG13180; YDBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              396 GVDGRLQAILQAHENELGDFVLHM 419
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                                                      33.8%;
llarity 44.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-331 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                             STANDARD;
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                                                                                   Local Similarity
ses 12; Conser
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P46045,
01-NOV-1995 (REL. 3
01-NOV-1995 (REL. 3
01-OCT-1996 (REL. 3
736 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-K12;
                                                                                                                                                                                                                                                                                                                T 5
YDBH_ECOLI
  SEQUENCE
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                                                            Query Match
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Gaps

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RESULT

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S FT

Length 442; 4; Indels

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REPEAT:
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IL11_MOUSE
P47873;
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                                                                                                                                    LYASE;
                                                                                                                                                             DOMAIN
                                                                                                                                                                                           REPEAT
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  SO THE FERT FROM THE FORT THE 
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-I- CATALYTIC ACTIVITY: ATP = 3',5'-CYCLIC AMP + PYROPHOSPHATE.

-I- IN CONTRAST TO YEAST CYCLASE, S.POWBE CYCLASE IS NOT LIKELY TO BE REGULATED BY RAS PROTEINS.
                                                                                                                                                                                                                                                                                                                                          UMETAMA T., HORIMOUCHI S.;
SUBMITTED (JAN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: INVOLVED IN THE REGULATION OF SECONDARY METABOLISM BY PHOSPHORYLATING, DO BOTH SER AND THR, THE AFSR GLOBAL REGULATORY PROFEIN INVOLVED IN THE CONTROL OF SECONDARY METABOLISM.
-!- PTM: ADTOPHOSPHORYLATED AT THR AND SER RESIDUES.
-!- SIMILARITY: WITH THE CONSERVED CATALITIC DOMAINS OF SER/THR-PROTEIN KINASES.
EMBL; D15062; E120137; -.
EMBL; D45382; G642157; -.
PROSITE; PS00107; PROTEIN_KINASE_ST; 1.
PROSITE; PS00118; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: THE REPEATED LEUCINE-RICH (LRR) SEGMENT IS FOUND IN MANY PROTEINS. NUMBER IN THIS PROTEIN: 22.
-!- SIMILARITY: BELONGS TO CLASS-3 OF ADENYLYL CYCLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YAMAWAKI-KATAOKA Y., TAMAOKI T., CHOE H.-R., TANAKA H., KATAOKA T., PROC. NATL. ACAD. SCI. U.S.A. 86:5693-5697(1989).
-!- FUNCTION: PLAYS ESSENTAL ROLES IN REGULATION OF CELLULAR METABOLISM BY CATALYSING THE SYNTHESIS OF A SECOND MESSENGER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-APR-1990 (REL. 14, CREATED)
01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL
                                                                                                                                                                                   STRAIN-A3(2);
MEDLINE; 94341568.
MATSUMOTO A., HONG S.K., ISHIZUKA H., HORINOUCHI S., BEPPU T.;
GENE 146:47-56(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE; 90046723.
YOUNG D., RIGGS M., FIELD J., VOJTEK A., BROEK D., WIGLER M.;
PROC. NATL. ACAD. SCI. U.S.A. 86:7989-7993(1989).
                                                                                                        PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; STREPTOMYCETACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
TRANSFERASE; SERINE/THREONINE-PROTEIN KINASE; ATP-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 65; DB 1; Length 799;
Pred. No. 5.25e+00;
7; Mismatches 8; Indels
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
SERINE/THREONINE PROTEIN KINASE AFSK (EC 2.7.1.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           545EE296 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCHIZOSACCHAROMYCES POMBE (FISSION YEAST)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     255 RPNPADLQAQLAPHLFGSGSDDSG 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83781 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 37.5%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                             COELICOLOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           799 AA;
                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 89345533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHORYLATION
                                                                             STREPTOMYCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYAA_SCHPO
P14605;
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SEQUENCE
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BINDING
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Gaps
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MORRIS J.C., FINNERTY H., BENNET F., TURNER K.J., WOOD C.R.;
EXP. HEMATOL. 24.1369-1376(1996).
- I- FUNCTION: THIS PROTEIN STIMULATES PLASMACYTOMA PROLIFERATION,
T-CELL-DEPENDENT DEVELOPMENT OF IMMUNOGLOBULIN-PRODUCING B
CELLS AND SYMERGIZES WITH IL-3 IN SUPPORTING MURINE
MEGAKARYOCYTE COLONY FORMATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
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Pred. No. 7.52e+00;
4; Mismatches 3; Indels
                                                                                       SYNTHESIS; MAGNESIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                       CEUCINE-RICH REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MW; 20E7D7D8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 65; DB 1; Lv
Pred. No. 5.25e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERLEUKIN-11.
1CB30772 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
10-VOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
INTERLEUKIN-11 PRECURSOR (IL-11).
-1- SIMILARITY: CONTAINS A PP2C-LIKE DOMAIN. EMBL; M26699; G173339; -. EMBL; M24942; G173379; -. PIR; A33988; A33589.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ż
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTI
                                                                                       CAMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                     LRR.
                                                                                                                                                                                                                                EMBL; U03421; G415554; -. MGD; MCI:107613; ILL11. CYTOKINE; GROWTH FACTOR; SIGNAL.
                                                                                                                                                                                                                LRR
                                                                                       LEUCINE-REPEAT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21522 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31.8%;
larity 53.3%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22
199 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 8; Conser
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu Jul 30 09:35:23 1998; MasPar time 5.13 Seconds 230.058 Million cell updates/sec Jular output not generated. ö

>US-08-938-548A-12 (1-28) from USO8938548A.pep 201 1 RPGPPGLQGRLQARGNHAAGILTM 28

Title: Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

140542 seqs, 42109429 residues

Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

sptrembl5
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_huhe 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Mean 30.024; Variance 52.279; scale 0.574 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	2.55e-01	3.68e-01	7.59e-01	3.12e+00	4.42e+00	6.22e+00	6.22e+00	6.22e+00	6.22e+00	6.22e+00	6.22e+00	6.22e+00	6.22e+00	6.22e+00	8.74e+00	8.74e+00	8.74e+00	8.74e+00	8.74e+00	8.74e+00
Description	TIGHT JUNCTION PROTEIN	PAR INTERACTING PROTEI	K+ CHANNEL BETA4 SUBUN	LEUCINE ZIPPER WITH BA	NUMA PROTEIN.	YONC PROTEIN.	MAXP1.	RNA POLYMERASE SIGMA F	ARTICULIN P60.	DNA POLYMERASE III TAU	HRPG.	DEOXYCYTIDINE-TRIPHOSP	UNKNOWN GENE.	T24D5.1.	RNA-DIRECTED DNA POLYM	THYROID HORMONE INDUCE				
Ð	095168	035821	P97382	091640	014980	031955	035141	P95644	059913	P77951	059813	059814	927212	045998	060245	027642	054224	922732	005804	091654
B B	4	2	10	12	~	σ	10	σ	σ	σ	σ	σ	m	σ	σ	σ்,	σ	ო	σ	12
å Query Match Length DB	1174	1277	249	331	2115	178	413	462	510	514	525	528	568	608	130	150	253	304	319	335
Query Match	37.8	37.3	36.3	34.3	33.8	33.3	33.3	33.3	33.3	33.3	33.3	33.3	33.3	33.3	32.8	32.8	32.8	32.8	32.8	32.8
Score	9/	75	73	69	68	67	. 67	67	67	67	67	67	67	67	99	99	99	99	99	99
Result	г	7	m	4	S	9	7	80	σ	10	11	12	13	14	15	16	. 17	18	19	20

8.74e+00 8.74e+00 8.74e+00 1.22e+01 1.22e+01 1.22e+01 1.71e+01 1.71e+01 1.71e+01 1.71e+01 1.71e+01 1.71e+01 1.71e+01 1.71e+01 1.71e+01 1.71e+01 1.71e+01 2.37e+01 2.37e+01 2.37e+01 2.37e+01 2.37e+01 3.29e+01 3.29e+01
HYPOTHETICAL 41.3 KD P CARA. H06001.2. PRISTINAMYCIN I SYNTHA RETINOID X RECEPTOR IN P160 MYB-BINDING PROTE FATTY ACID SYNTHASE (E PUTATIVE SIGMA-54 DEPE OMF23. HOMODA HYDROLASE. ORF328 (FRAMENT). PROTEIN-TYROLASE. PROTEIN-TYROLASE. PROTEIN-TYROLASE. PROTEIN-TYROLASE. PROTEIN-TYROSINE PHOSP KM-102-DERLYED REDUCTA PUTATIVE EPIDERMAL CEL FROM BASES 1860594 TO NODO. HYPOTHETICAL 85.5 KD P EXTRACELLULAR MATRIX P KIAAO310. TYLACTONE SYNTHASE MOD POLYRETIDE SYNTHASE MOD POLYRETIDE SYNTHASE MOD C-SRC TYROSINE KINASE. A TYPE IV COLLAGEN (FR
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ALIGNMENTS

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	CIA;		
1 95168 95168; PRELIMINARY; PRT; 1174 P 95168; CREMBLREL. 02, CREATED) 1-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE 1-7AN-1998 (TREMBLREL. 05, LAST ANNOTATIC 1-GTT JUNCTION PROTEIN. 0-2. ANIS FAMILIARIS (DOG).	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; CARNIVORA. [1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE; 94179414. MEDLINE; 94179414. J. SCALL BIOL. 124:949-961(1994).	SEQUENCE FROM N.A. MEDILINE, 96211547. BERATCH M., JESAITIS L.A., GALLIN W., GOODENOUGH D.A., STEVENSON B.R.; J. BIOL. CHEM. 271:25723-25726(1996). [3] SEQUENCE FROM N.A. GOODENOUGH D.A.; SUBMITTED (MAR-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.	L41 BEATCH M.; BEATCH M.; BEATCH M.; SUBMITTED (AUG-1996) TO EMBL/GENBANK/DDBJ DATA BANKS. EMBL; L27152; G1536970; EMBL; L27152; G1536970; SEQUENCE 1174 AA; 132085 MW; 2FA16883 CRC32; Query Match 37.88; Score 76; DB 4; Length 1174; Best Local Similarity 32.18; Pred. No. 2.55e-01; Matches 9; Conservative 12; Mismatches 7; Indels 0
RESULT ID DO DT O DT O DT O GN C	R R R R R C C C	R R R R R R R R R R R R R R R R R R R	RAN RAN RAN SQ Qu Mai

268 RSPSPELRGRPDHAGOPDSDRPIGVLLM 295

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PRELIMINARY;

PRT; 1277 AA.

RESULT 2 ID 035821

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MOESTL D., NAKAI S., NOBACK M., NOONE D., O'REILLY M., OGRAR K.,
GIWARA A., OUDGGA B., PARK S.H., PARRO V., POHL T.M., PORTETELLE D.,
RAPOPORT G., REY M., REYNOLDS S., RIEGER M., RIVOLTA C., ROCHA E.,
RAPOPORT G., REY M., SADAIE Y., SATO T., SCANIAN E., SCHIELE S.,
A SCHROETER R., SOOFFONE F., SETGIGHIA I., SHOWN S.H., SEROR S.J.,
A TAKAHASHI H., TAKEMARU K., SOLDO B., SOROKIN A., TACCONI E., TAKAGI T.,
A TAKAHASHI H., TAKEMARU K., TAKEGOTH M., TAMAKOSHI A., TANAKA
A VANNIER F., VASSAROTTI A., TAKEGOTH M., TAMAKOSHI A., TANAKA
A WANIER F., VASSAROTTI A., VIARI A., WAMBUT R., WEDLER H.,
A KASUMOTO K., YATA K., YOSHIDA K., YOSHIKAMA H.F., ZUMSTEIN E.,
A YASUMOTO K., YATA K., YOSHIDA K., YOSHIKAMA H.F., ZUMSTEIN E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RATIUS NORVEGICUS (RAI).
EUKARYOIA; METAZOA; CHORDAIA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
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Pred. No. 6.22e+00;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                        Length 178;
                                                                                                                                                                                                                                                                                                                                  7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-ATCC33209;
BARRIL A., CONCHA M.I., FIGUEROA J., LEON G.;
SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                              STRAIN=168;
KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; 299115; E1183561; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
SLEPNEV V.I., DE CAMILLI P.V.;
SUENHITED (0-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL, AF001251; G2459833; -.
SEQUENCE 413 Aa; 46679 MW; 69A87FCC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EUBACTERIA; FIRMICUTES; ACTINOMYCETES; RENIBACTERIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-WAY-1997 (TREMBLREL. 03, CREATED)
01-WAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                    33.3%; Score 67; DB 9; L
larity 45.0%; Pred. No. 6.22e+00;
Conservative 4; Mismatches 7
                                                                                                                                                                                                                                                                                CA7B8ED0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                         413 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  462 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY; PRT;
                                                                                                                                                                                                                                                                             19609 MW;
                                                                                                                                                                                                                                                                                                                                                            1 MATRLQKALTEVGNHTTGNL 20
                                                                                                                                                                                                                                                                                                                                                                            : |||: | |||:| |
7 LQGRLQRLLQANGNHAAGIL 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                05,
05,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNA POLYMERASE SIGMA FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jery Match
Best Local Similarity 69.2%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RENIBACTERIUM SALMONINARUM
                                                                                                                                                                                      NATURE 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1998 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76 RPVRPGLQQRLRR 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 AA;
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                              SEQUENCE
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P95644;
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Matches
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GENE 153:41-48(1995).

- FORDION THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES
- FORDITON: THE SIGMA FACTOR IS AN INITIATION SITES AND THEN IS RELEASED.

EMBL: X75922, G561664; -.

PROSITE; PS00715; SIGMA70_1; 1.

PROSITE; PS00716; SIGMA70_2; 1.

TRANSCRIPTION REGULATION; SIGMA FACTOR; DNA-DIRECTED RNA POLYMERASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SHINKAWA H., HATADA Y., OKADA M., KINASHI H., NIMI O.;
J. BIOCHEM. 118:494-499(1995).
- FUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES
- ATTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES AND
-!- FUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES ATTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES AND THEN IS RELEASED.
                                                                                                        EMBL; Y10835; E294130; -
PROSITE; PS00715; SIGMA70_1; 1.
PROSITE; PS00716; SIGMA70_2; 1.
TRANSCRIPTION REGULATION; SIGMA FACTOR; DNA-DIRECTED RNA POLYMERASE;
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PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; STREPTOMYCETACEAE
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PROKARYOTA; FIRMICUTES; ACTINOMYCETALES; STREPTOMYCETACEAE
                                                                                                                                                                                                                                                                                                                                                                     Length 462;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
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01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TREMBLREL. 02, LAST SEQUENCE UPDATE)
(TREMBLREL. 05, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                          Score 67; DB 9; LA
Pred. No. 6.22e+00;
11; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 67; DB 9; L
Pred. No. 6.22e+00;
                                                                                                                                                                                                                                                                                                462 AA; 50504 MW; E54BBFE5 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              510 AA; 55795 MW; C3CB64EB CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           390 LQEQLHSVLDTLSEREAGVVAM 411
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LQGRLQRLLQANGNHAAGILTM 28
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llarity 31.8%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                              33.3%;
imilarity 31.8%;
7; Conservative
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EMBL; L08071; G1617256; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1997 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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MEDLINE; 95189101
MARCOS A.T., DIEZ
                                                                                                                                                                                                                                                            DNA-BINDING
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01-JAN-1998
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1D 059913
1D 059913
1D 059913
1D 01-NOV-11
1D 01
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P77951;
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GN HRPG.
OS PSEUDOMONAS SYRINGAE.
OC PROMARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI; OC PSEUDOMONADACEAE.
RN [1]
RP SEUDOMONADACEAE.
RX #GILINE: 96025090.
RX #EDLINE: 96025090.
RA HUANG H.C., LIN R.H., CHANG C.J., COLLMER A., DENG W.L.; R. HUANG H.C., LIN R.H., CHANG S.J., COLLMER A., DENG W.L.; R. MOL. FLANT MICROBE INTERACT. 8:733-746(1995).
DR EMBL; U25813; G818900.
SQ SEQUENCE 130 AA; 13950 MW; 5CDEACF8 CRC32;
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Query Match 32.8%; Score 66; DB 9; Length 130;
Best Local Similarity 40.7%; Pred. No. 8.74e+00;
Matches 11; Conservative 8; Mismatches 7; Indels 1; Gaps
Db 80 PGPCGLADLINRL-ESLANQRAALLS1 105

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80 PGPCGLADLLNRL-ESLANGRAALLSL 105 ||| || || || || :::|:|::|:: 2 PGPPGLQGRLQRLLQANGNHAAGILTM 28 Search completed: Thu Jul 30 09:35:47 1998 Job time: 24 secs.

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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu Jul 30 09:27:56 1998; MasPar time 8.78 Seconds 589.674 Million cell updates/sec Run on:

>US-08-938-548A-10 (1-123) from US08938548A.pep pular output not generated. Title:

1 VPWAAVTLLLLLLLPPALLS......GRGCPTVTTTALAPRGGSGV 123 Description: Perfect Score: Sequence:

Scoring table:

PAM 150 Gap 11

Minimum Match 0% Listing first 45 summaries Post-processing:

140542 seqs, 42109429 residues

Searched:

Database:

sptrembl5
1:sp_fung1 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Mean 39.425; Variance 86.061; scale 0.458

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

2.41e-02 5.93e-02 2.57e-01 8.09e-01 1.07e+00 1.42e+00 47e+00 Pred. No ACYLOXYACYL HYDROLASE.
LEUCINE ZIPPER WITH BA
TIGHT JUNCTION PROTEIN
PROLINE AND LEUCINE-R
CYCLOOXYGENASE ISOFORM
CYCLOOXYGENASE 1. SORTILIN PRECURSOR.
PROSTAGLANDIN H SYNTHA
HYPOTHETICAL 23.1 KD P
THYROLD HORMONE INDUCE
HYPOTHETICAL 25.9 KD P
DNA BINDING PROTEIN EI HYPOTHETICAL 74.6 KD P PLATELET GLYCOPROTEIN FRIZZLED PROTEIN HOMOL PROSTAGLANDIN ENDOPERO SIMILARITY TO MOUSE SM HYPOTHETICAL 48.1 KD P NB-2. PORCINE MEMBRANE COFAC Description 023352 008770 008463 035298 091640 09164 0631051 0633821 06363831 062731 P72841 P97527 002839 091654 005582 090491 015122 018780 Query Match Length DB 12921 4 5 0 m 335 252 252 583 599 1238 410 410 363 106 602 602 833 602 226 1006 993 993 993 993 993 993 887 887 887 887 887 887 887 887 Mo.

9.56e+00	1.25e+01	1.25e+01	1.25e+01	1.25e+01	1.25e+01	1.25e+01	1.62e+01	1.62e + 01	1.62e+01	1.62e+01	1.62e+01	1.62e+01	1.62e+01	1.62e+01	2.10e+01	2.10e+01	2.10e+01	2.10e+01	2.10e+01	2.72e+01	2.72e+01	2.72e+01	2.72e+01	2.72e+01
RNA-DEPENDENT RNA POLY	ANION EXCHANGER ISOFOR	108 PROTEIN PRECURSOR.	HYPOTHETICAL 30.9 KD P	HYPOTHETICAL 72.6 KD P	ANION EXCHANGER 2 A (F	DIACYLGLYCEROL KINASE	3' ORF.	NEUROVIRULENCE FACTOR.	MYOMODULIN (FRAGMENT).	MYOMODULIN PRECURSOR (LECITHIN: CHOLESTEROL A	MALTASE-LIKE PROTEIN A	PCBR.	GUANYLATE CYCLASE E.	HYPOTHETICAL 27.7 KD P	MYOMODULIN NEUROPEPTID	FROM BASES 1860594 TO	VERY LARGE TEGUMENT PR	TYLACTONE SYNTHASE MOD	FERRIC ENTEROBACTIN TR	FROM BASES 2573751 TO	F18A12.4 PROTEIN.	GUANYLATE CYCLASE ISOF	MYOSIN.
083101	060471	043495	033285	065568	060470	000542	061639	012396	027916	007974	035849	017021	P72405	019179	P95156	025413	P76237	P89459	033956	046729	P76559	016791	002809	039160
11	2	ω	σ	11	10	~	10	11	m	m	10	m	σ	4	9	m	6	11	σ	σ	0	m	4	ω
878	84	102	277	701	729	1117	147	248	329	370	440	498	551	1109	264	350	556	3122	3729	40	347	734	1110	1520
9.5	9.3	9.3	9.3	9.3	9.3	9.3	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.1	9.1	9.1	9.1	9.1	0.6	9.0	9.0	9.0	9.0
82	84	84	84	84	84	84	83	83	83	83	83	83	83	83	82	82	82	82	82	81	81	81	81	81
21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

95 94 GA ŏ

655 SP 656

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Gaps

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RATIUS NORVEGICUS (RAI).
EUKARYOIA; METAZOA; CHORDAIA; VERIEBRAIA; IETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                            MEDLINE; 94099619.
FENG L., SUN W., XIA Y., TANG W.W., CHANMUGAM P., SOYOOLA E., WILSON C.B., HANNG D., ACH. BIOCHEM. BIOPHYS, 307:361-368(1993).
EMBL; S67721; G460556; -.
NOM_TER 602 602
SEQUENCE 602 AA; 69158 MW; 4EBDC921 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-FISHER 344;
FENG L., SUN W., XIA Y., TANG W.W., CHANMUGAM P., SOYOOLA E., WILSON C.B., HWANG D.;
MILSON C.B., BIOPHYS. 307:0-0(0).
EMBL; U03388; G415638;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01, CREATED)
01, LAST SEQUENCE UPDATE)
01, LAST ANNOTATION UPDATE)
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 2.47e+00;
5; Mismatches 6
                                                                                                                                                                                                                                                                                             Score 91; DB 10;
Pred. No. 1.87e+00;
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Pred. No. 1.87e+00;
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; D2E351B9 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                8 LLLLLLLPPA--LLS-LGVDAQPLPDCC 32
                                                                                                                                                                                                                                                                                                                                                                                                     13 LLLLLLPPPPVLLTDAGVPSPVIP-CC 39
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92408 MW;
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03,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 10.1%;
Best Local Similarity 57.1%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                             Query Match 10.1%;
Best Local Similarity 57.1%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 10.0%;
Best Local Similarity 53.3%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ULT 10
099523
099523, PRELIMINAR
099523, 01-MAY-1997 (TREMBLREL. 0
01-MAY-1997 (TREMBLREL. 0
01-JAN-1998 (TREMBLREL. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
01-NOV-1996 (TREMBLREL.
CYCLOOXYGENASE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33
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833 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SORTILIN PRECURSOR.
     EUTHERIA; RODENTIA
                                                           FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DET 9
Q63684
Q63684;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
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Q41051;
Q41051;
O1-NOY-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
O1-NOY-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
PROLINE- AND LEUCINE-RICH PROTEIN.
PISUM SATIVUM (CARDEN PEA).
EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE; FABALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            266 RSRSPSPELRGRPDHAGQPDSDRPIGVLLMKSKANEEYGLRLGSQIFIKQMTRTALATKD 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
CYCLOOXYGENASE ISOFORM COX-1 (FRAGMENT).
RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA: CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALLA;
EUTHERIA; CARNIVORA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 10.2%; Score 92; DB 8; Length 106; Best Local Similarity 61.9%; Pred. No. 1.42e+00; Matches 13; Conservative 4; Mismatches 4; Indels
                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE; 96421547.
BEATLINE, JESAITIS L.A., GALLIN W., GOODENOUGH D.A.,
STEVENSON B.R.;
J. BIOL. CHEM. 271:25723-25726(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RODRIGUEZ-CONCEPCION M., PEREZ-GARCIA A., BELTRAN J.; SUBMITTED (MAR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS. EMBL; Z67873; E208986; - EMBL; Z67873; E208986; - EMBL; Z67873; E360UENCE 106 AA: 11828 MW; A45AD924 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BEATCH M.;
SUBMITTED (ADC-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; L27152; G1536970; -...
SEQUENCE 1174 AA: 132085 MW; 2FA16B83 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                        GOODENOUGH D.A.; SUBMITTED (MAR-1994) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    602 AA
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                                                                              SEQUENCE FROM N.A.
MEDLINE; 94179414.
JESAITIS L.A., GODENOUGH D.A.;
J. CELL BIOL. 124:949-961(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 ILLLLLPPPLLLLLMRPLPL 92
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Best Local Similarity 29.0%;
Matches 18; Conservative
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  3; Gaps
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01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DNA BINDING PROTEIN E12.
BRACHTDANIO (ZEBRAFISH) (ZEBRA DANIO).
EUKARNOTA: METAZOA: CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OSTEICHTHYES; ACTINOPTERYGII; CYPRINIFORMES.
19; Conservative 15; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-WT; TISSUE-WHOLE EMBRYO;
MEDLINE; 95001558.
WUELBECK C., FROMENTAL-RAMAIN C., CAMPOS-ORTEGA J.A.;
EMBL; X76997; GS09754; -.
                                                                                                                                                                                                                           (TREMBLREL. 01, CREATED)
(TREMBLREL. 01, LAST SEQUENCE UPDATE)
(TREMBLREL. 01, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      583 AA; 62625 MW; A874D9E2 CRC32;
                                                                                                                                                                                 583 AA.
                                                                                                                                                                                 PRT;
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Matches
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Gaps

Query Match
9.7%; Score 87; DB 12; Length 583;
Best Local Similarity 38.6%; Pred. No. 5.60e+00;
Matches 17; Conservative 10; Mismatches 15; Indels

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Search completed: Thu Jul 30 09:28:17 1998 Job time : 21 secs.

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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu Jul 30 09:27:25 1998; MasPar time 5.12 Seconds 602.279 Million cell updates/sec Run on:

pular output not generated.

>US-08-938-548A-10 (1-123) from USO8938548A.pep 899 1 VPWAAVTLLLILLLPPALLS......GRGCPTVTTTALAPRGGSGV 123 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

69111 seqs, 25083644 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

swiss-prot35 1:swiss1

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 41.408; Variance 75.349; scale 0.550

SUMMARIES

Pred. No.	1.48e-02	7.91e-02	7.91e-02	7.91e-02	7.91e-02	3.99e-01	7.51e-01	1.03e+00	1.03e+00	1.90e+00	1.90e+00	1.90e+00	1.90e+00	2.57e+00	2.57e+00	2.57e+00	2.57e+00	3.48e+00	3.48e+00	3.48e+00	3.48e+00	3.48e+00	3.48e+00
Description	SECRETIN PRECURSOR (FR	FIBULIN-1, ISOFORM A P	FIBULIN-1, ISOFORM B P	FIBULIN-1, ISOFORM C P	FIBULIN-1, ISOFORM D P	PHOSPHATIDYLCHOLINE-ST	ATRIAL NATRIURETIC PEP	4-1BB LIGAND (4-1BBL).	PHOSPHATIDYLCHOLINE-ST	HYPOTHETICAL PROTEIN H	PHOSPHATIDYLCHOLINE-ST	SEC14 CYTOSOLIC FACTOR	COMPLEMENT C3 PRECURSO	PLACENTAL LACTOGEN I P	LIPASE 1 PRECURSOR (EC	FERRIC ENTEROBACTIN TR	FIBRIL-FORMING COLLAGE	E PROTEIN.	LYSIS PROTEIN.	EPHRIN-A3 PRECURSOR (E	COMPLEMENT C1Q SUBCOMP	LIPASE 3 PRECURSOR (EC	HYPOTHETICAL 36.0 KD P
a	SECR_PIG	FBLA_HUMAN	FBLB_HUMAN	FBLC_HUMAN	FBLD_HUMAN	LCAT_HUMAN	ANPA_HUMAN	41BL_HUMAN	LCAT_MOUSE	YCEC_HAEIN	LCAT_PAPAN	SC14_YARLI	CO3_RAT	PLC1_BOVIN	LIP1_PSYIM	FEPD_ECOLI	CAFF_RIFPA	VGE_BPS13	VGE_BPPHX	EFA3_HUMAN	C1QB_HUMAN	LIP3_MORSP	YCEC_ECOLI
DB	-	-	H	-			Н	-	-	-		Н	-1	Н	н	~	н	1	~	-	-	Н	Н
% Query Match Length DB	131	266	601	683	703	440	1061	254	438	322	440	497	1663	236	317	334	1027	90	90	238	251	315	319
& Query Match	11.2	10.7	10.7	10.7	10.7	10.1	9.9	9.6	8.6	9.6	9.6	9.6	9.6	9.5	9.5	9.5	9.5	9.3	9.3	9.3	9.3	9.3	9.3
Score	101	96	96	96	96	91	89	88	88	98	98	86	86	82	82	82	82	84	84	84	84	84	84
Result No.		7	m	₹		9	7	œ	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

3.48e+00 3.48e+00	3.48e+00	3.48e+00	4.69e+00	4.69e+00	4.69e+00	4.69e+00	4.69e+00	4.69e+00	4.69e+00	4.69e+00	4.69e+00	4.69e+00	4.69e+00	4.69e+00	4.69e+00	4.69e+00	4.69e+00	6.30e+00	6.30e+00	6.30e+00
GTPASE ACTIVATING PROT	PROTEIN-TYROSINE PHOSP	TALIN.	PLATELET GLYCOPROTEIN	OXALATE OXIDASE PRECUR	SL CYTOKINE PRECURSOR	INFECTED CELL PROTEIN	INFECTED CELL PROTEIN	INFECTED CELL PROTEIN	PHOSPHATIDYLCHOLINE-ST	PHOSPHATIDYLCHOLINE-ST	HYPOTHETICAL 59.6 KD P	SERUM ALBUMIN PRECURSO	CELL DIVISION PROTEIN	TRANS-ACTING TRANSCRIP	TRANS-ACTING TRANSCRIP	PROTEIN-TYROSINE PHOSP	ANGIOTENSIN-CONVERTING	INFECTED CELL PROTEIN	METALLO-BETA-LACTAMASE	ADENYLATE CYCLASE, TYP
RN_DROME	PIPX MOUSE	TALI_MOUSE	GPBB_PAPCY	OXO2_HORVU	FL3L_HUMAN	ICP3_HSV11	ICP3_HSV1D	ICP3_HSV1F	LCAT_RABIT	LCAT_RAT	YABK_ECOLI	ALBU_CHICK	FTSH_PORPU	ICPO_HSVBJ	ICPO_HSVBK	PTPX_RAT	ACE_RABIT	ICP3_HSV1N	BLA1_XANMA	CYA6_MOUSE
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e.e.	۳. م	9.3	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.5	9.1	9.1	9.1
8 8 4 4	84	84	83	83	83	83	83	83	83	83	83	83	83	83	83	83	83	82	82	82
24	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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MEDLINE: 89354537.

MEDLINE: 89354537.

MEDLINE: 89354537.

MEDLINE: 80354537.

CELL 58:623-629(1989).

-!- SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX.

-!- ALTERNATIVE PRODUCTS: FOUR FORMS OF FIBULIN-1; A (AC P23142), B

(AC P23143), C (SHOWN HERE) AND D (AC P37888); DIFFERING ONLY IN

THEIR C-TERMINAL REGIONS, ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- SIMILARITY: CONTAINS 9 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X53743; G31419; -..

EMBL; X53745; G31419; -..

PIR; A32826; A32826

MIM; 135820; -..

PROSITE; PS00010; ASX_HYDROXYL; 4..

PROSITE; PS010179; ANAPHYLATOXIN_1; 3..

PROSITE; PS01178; ANAPHYLATOXIN_2; 3..

PROSITE; PS01186; EGF_2; 3..

PROSITE; PS01187; EGF_CA; 8..

SIGNAL; ALTERNATIVE SPLICING; GLYCOPROTEIN; EXTRACELLULAR MATRIX; REPEAT; PLASMA; EGF-LIKE DOMAIN; CALCIUM-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 96; DB 1; Length 601,
Pred. No. 7.91e-02;
3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FIBULIN-1, ISOFORM C.
3 X ANAPHYLATOXIN REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE; 91100426.
ARGENS W.S., TRAN H., BURGESS W.H., DICKERSON K.;
J. CELL BIOL. 111:3155-3164(1990).
                                                                                                                                                                                                                                                                                                                                                                                                               -> S (IN REF. 2).
(-> SH (IN REF. 2)
3A6E492B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEBC_HUMAN STANDARD; PRT; 683 AA. P23144; 01-NOV-1991 (REL. 20, CREATED) 01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE) 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE) PIBULIN-1, ISOFORM C PRECURSOR.
                                                               SIMILARITY.
SIMILARITY.
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BY SIMILAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 VPLPLLLGGLALLAAGVDADVLLEACC 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 VTLILLILLEPPALLSLGVDAQPLPD-CC 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MW.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
10.7%;
Best Local Similarity 57.1%;
Matches 16; Conservative
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(HUMAN)
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36 30
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CHAIN
DOMAIN
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3 X ANAPHYLATOXIN REPEATS.
ANAPHYLATOXIN-LIKE 1.
ANAPHYLATOXIN-LIKE 1.
ANAPHYLATOXIN-LIKE 2.
ANAPHYLATOXIN-LIKE 3.
EGF-LIKE 1.
EGF-LIKE 2.
EGF-LIKE 4. CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 5. CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 6. CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 6. CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 6. CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 7. CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 9. CALCIUM-BINDING (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                        MEDILIE; 9935437.

ARGRAVES W.S., DICKERSON K., BURGESS W.H., RUOSLAHTI E.;

CELL 58:623-629(1989).

-! SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX.
-! ALTERNATIVE PRODUCTS: FOUR FORMS OF FIBULIN-1; A (AC P23142), B (SHOWN HERE). C (AC P2144) AND D (AC P37889); DIFFERING ONLY IN THEIR C-TERMINAL REGIONS, ARE PRODUCED BY ALTERNATIVE SPLICING.
-! SIMILARITY: CONTAINS 3 ANAPHYLATOXIN-LIKE DOMAINS.
-! SIMILARITY: CONTAINS 9 EGF-LIKE DOMAINS.
-! SIMILARITY: CONTAINS PEGF-LIKE DOMAINS.
-! SIMILARITY: OF PRODUCED BY ALTERNATIVE SPLICING.
-! SIMILARITY: CONTAINS PEGF-LIKE DOMAINS.
-! SIMILARITY: OF PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PSOU010; ASX_HYDROXYL; 4.
PROSITE; PSOU012; EGF_1; FALSE_NEG.
PROSITE; PSO1177; ANAPHYLATOXIN_1; 3.
PROSITE; PSO1188; ANAPHYLATOXIN_2; 3.
PROSITE; PSO1187; EGF_2; 3.
PROSITE; PSO1187; EGF_2; 8.
SIGNAL; ALTERNATIVE SPLICING; GLYCOPROTEIN; EXTRACELLULAR MATRIX; REPEAT; PLASMA; EGF-11KE DOWAIN; CALCIUM-BINDING.
                                                                                                                                   HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                            SEQUENCE FROM N.A.

BEDLINE; 91100426.

ARGRAVES W.S., TRAN H., BURGESS W.H., DICKERSON K.;
                  01-NOV-1991 (REL. 20, CREATED)
01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
FIBULIN-1, ISOFORM B PRECURSOR.
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DOMAIN
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Gaps

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VARIANT ARG-170
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                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                        20-MAR-1987 (REL. 04, CREATED)
20-MAR-1987 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43)
(LECITHIN-CHOLESTEROL ACYLTRANSFERASE) (PHOSPHOLIPID-CHOLESTEROL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANTS ILE-147 AND MET-371.
MEDLINE; 92147865.
KLEIN H.-G., LOHSE P., PRITCHARD P.H., BOJANOVSKI D., SCHMIDT H.,
BREWER H.B. JR.;
J. CLIN. INVEST. 89:499-506(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
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MEDILINE; 87137578.
YANG C., MANOGIAN D., PAO Q., LEE F., KNAPP R.D., GOTTO A.M.
POWNALL H.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G.D., WATERFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ROGNE S., SKRETTING G., LARSEN F., MYKLEBOST O., MEVAG B., CARLSON L.A., HOLMQUIST L., GJONE E., PRYDZ H.; BIOCHEM. BIOPHYS. RES. COMMUN. 148:161-169(1987).
                                                                           Score 96; DB 1; Length 703; Pred. No. 7.91e-02; 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCHINDLER P.A., SETTINERI C.A., COLLET X., FIELDING C.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE; 86205950.
MCLEAN J., FIELDING C., DRAYNA D., DIEPLINGER H., BAER
HENZEL W., LAWAN R.;
PROC. NATL. ACAD. SCI. U.S.A. 83:2335-2339(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE, 87091568.
MECLEND J. WION K., DRAYNA D., FIELDING C., LAWN R.;
NUCLEIC ACIDS RES. 14:9397-9406(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANT LEU-34.
MEDLINE; 92134273.
SKRETING G., PRYDZ H.;
BIOCHEM. BIOPHYS. RES. COMMUN. 182:583-587(1992).
                   539 POTENTIAL.
77274 MW; F0D06821 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 88050946.
TATA F., CHAVES M.E., MARKHAM A.F., SCRACE G
MCINNYRE N., WILLIAMSON R., HUMPHRIES S.E.;
BIOCHIM. BIOPHYS. ACTA 910:142-148(1987).
                                                                                                                                                                                                                                                                          440 AA
   POTENTIAL
                                                                                                                                                                             6 VTLLLILLEPPALLSLGVDAQPLPD-CC 32
                                                                                                                                                         10 VPLPLLLGGLALLAAGVDADVLLEACC 37
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J. BIOL. CHEM. 262:3086-3091(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BURLINGAME A.L.;
PROTEIN SCI. 4:791-803(1995)
                                                                           Query Match 10.7%;
Best Local Similarity 57.1%;
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                                                                                                                       16; Conservative
                                                                                                                                                                                                                                                                      STANDARD;
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535 5
539 5
703 AA;
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P04180;
                     CARBOHYD
SEQUENCE
   CARBOHYD
                                                                                                                     Matches
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ID LC
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FUNE H., ASSMANN G.;
HUM. MUTAT. 8:79-82[1996].
-1-FUNCTION: CENTRAL ENZYME IN THE EXTRACELLULAR METABOLISM OF PLASMA
-1-FUNCTION: CENTRAL ENZYME IN THE EXTRACELLULAR METABOLISM OF PLASMA
-1-EUPOPROTEINS. AMONG OTHERS SUBSTRATES IT ESTERIFIES THE FREE
CHOLESTEROL TRANSPORTED IN PLASMA LIPOPROTEINS.
-1-CATALYTIC ACTIVITY: PHOSPHATIDYLCHINE, STEROL = STEROL ESTER +
1-ACYLCHYCEROPHOSPHOGPHORIUR (PALMITOYL, OLEOYL, AND LINOLEOYL CAN
BE TRANSFERRED; A NUMBER OF STEROLS, INCLUDING CHOLESTEROL, CAN
MEDLINE; 90316533.
TARAMELLI R., PONTOGLIO M., CANDIANI G., OTTOLENGHI S., DIEPLINGER H.,
CATAPANO A., ALBERS J., VERGANI C., MCLEAN J.;
HUM. GENET. 85:195-199(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GERDES U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACT AS ACCEPTOR).
ENZYME REGULATION: APOLIPOPROTEIN A-I IS A POTENT ACTIVATOR FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- SIMILARITY: PARTIAL WITH LIPASES (PANCREATIC, GASTRIC, HEPATIC,
                                                                                                                                                                                                                                       SAKUMA M., MURAYAMA N., SHIMANO H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 91315467.
MAEDA E., NAKA Y., MATOZAKI T., SAKUMA M., AKANUMA Y., YOSHINO G.,
KASUGA M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HOERL G., GIESSAUF W., KOSTNER G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 95221171.
WIEBUSCH H., CULLEN P., OWEN J.S., COLLINS D., SHARP P.S., FUNKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 93163362.
FUNE H., VON ECKARDSTEIN A., PRITCHARD P.H., HORNBY A.E.,
WIEBUSCH H., MOTTI C., HAYDEN M.R., DACHET C., JACOTOT B., GER
FAERGEMAN O., ALBERS J.J., COLLEONI N., CATAPANO A., FROHLICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- DISEASE: DEFECTS IN LCAT ARE THE CAUSE OF NORUM AND FISH DISEASES.
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OWEN J.S., WIEBUSCH H., CULLEN P., WATTS G.F., LIMA V.L.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANTS THR-117; TRP-159; CYS-182; PRO-233 AND MET-345.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        SKRETTING G., BLOMHOFF J.P., SOLHEIM J., PRYDZ FEBS LETT. 309:307-310(1992).
                                                                                                                                                                                                                                    GOTODA I., YAMADA N., MURASE I., SAKUWA M., MUI
KOZAKI K., ALBERS J.J., YAZAKI Y., AKANUMA Y.;
LANCEI 338:778-781(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
EMBL; M12625; G307117; -.
EMBL; X06537; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 93305754.
HILL J.S., O K., WANG X., PRITCHARD P.H.;
BIOCHIM. BIOPHYS. ACTA 1181:321-323(1993).
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EMBL; M26568; GB7025; -
EMBL; X04981; G34287; -
EMBL; M17959; G386858; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLIN. INVEST. 91:677-683(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HUM. MOL. GENET. 4:143-145(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT HIS-164.
MEDLLINES, 95331753.
STEYRER E., HAUBENWALLNER S.,
ZECHNER R.;
                                                                                                                                                              VARIANTS LYS-252 AND ILE-317. MEDLINE; 92016763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUM. GENET. 96:105-109(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A00571; XXHUN.
PIR; A29661; A29661
                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 92387377.
                                                                                                                                                                                                                                                                                                                                                                          VARIANT LYS-276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THIS ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT ILE-317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANT SER-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASSMANN G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASSMANN G.
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PASTEURELLACEAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LT 11
LCAT_PAPAN
Q08758;
                                                                                                                                                                                                                                                                                             LT 10
YCEC_HAEIN
P44433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                 SULTANDA SUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCC SERVICE SE
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MERONI G., MALGARETTI N., MAGNACHI P., TARAMELLI R.;
SUBMITTED (MAY-1992) TO EMBL/GENBANK/DDBJ DATA BANKS.
-1- FUNCTION: CENTRAL ENZYME IN THE EXTRACELLULAR METABOLISM OF PLASMA LIPOPROTEINS. AMONG OTHER SUBSTRATES IT ESTERIFIES THE FREE
                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHOLESTEROL TRANSPORTED IN PLASMA LIPOPROTEINS.

- CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + STEROL = STEROL

1-ACYLGIVCEROPHOSPHOSPHOLINE (PALMITOYL, OLEOYL, AND LINGLEOYL CAN
BE TRANSFERRED; A NUMBER OF STEROLS, INCLUDING CHOLESTEROL, CAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00120; LIPASE_SER; 1.
TRANSFERASE; ACYLTRANSFERASE; LIPID METABOLISM; GLYCOPROTEIN; SIGNAL.
-!- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, PLACENTA, LUNG, SKELETAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LECITHIN-CHOLESTEROL ACYLTRANSFERASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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-1- ENZYME REGULATION: APOLIPOPROTEIN A-I IS A POTENT ACTIVATOR FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- SIMILARITY: PARTIAL WITH LIPASES (PANCREATIC, GASTRIC, HEPATIC,
LINGUAL, LIPOPROTEIN, BACTERIAL, ETC.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1990 (REL. 15, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
(LECITHIN-CHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43)
(LECITHIN-CHOLESTEROL ACYLTRANSFERASE) (PHOSPHOLIPID-CHOLESTEROL ACYLTRANSFERASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WARDEN C.H., LANGNER C.A., GORDON J.I., TAYLOR B.A., MCLEAN J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ï
                                                            BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                      Score 88; DB 1; Length 254;
Pred. No. 1.03e+00;
4; Mismatches 1; Indels
                                                                                  EMBL; U03398; G571323; -.
PROSITE; PS00251; TNF_1; 1.
PROSITE; PS50049; TNF_2; 1.
CYTOKINE; TRANSMEMBANE; GLYCOPROTEIN; SIGNAL-ANCHOR.
DOMAIN 1 28 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
9E6B904A CRC32;
                                                                                                                                                                                                                                                                                                                               C68C1B27 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    438 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . BIOL. CHEM. 264:21573-21581(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1990 (REL. 15, CREATED)
                                                                                                                                                                                                                                                                                                                               26624 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49765 MW;
                                                                                                                                                                                                                                                                                                                                                                                         9.88;
                                                                                                                                                                                                                                                                                                                                                                                                                    66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VPWAAVT-LLLLLLLPPA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 LPWALVAGLLLLLLLAAA 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                   12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; J05154; G293697; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                         -!- SIMILARITY: BELONC
EMBL; U03398; G571323;
                           MUSCLE AND KIDNEY
                                                                                                                                                                                                                                                                                                                               254 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                408
438 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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MGD; MGI:96755; LCZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90094326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LCAT_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LUSIS A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACT_SITE
DISULFID
DISULFID
                                                                                                                                                                                                                                          TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
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                                                                                                                                                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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HIXSON J.E., DRISCOLL D.M., BIRNBAUM S., BRITTEN M.L.;
GENE 128:295-2991993).
-1- FUNCTION: CENTRAL ENZIME IN THE EXTRACELLULAR METABOLISM OF PLASMA
LIPOPROTEINS. AMONG OTHER SUBSTRATES IT ESTERIFIES THE FREE
CHOLESTEROL TRANSPORTED IN PLASMA LIPOPROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAEMOPHILUS INFLUENZAE.
PROKARYOTA: GRACILICUTES; SCOTOBACTERIA; FACULTATIVELY ANAEROBIC RODS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KERLAVAGE A.R., BULT C.J., TOMB J.-F., DOGGHERTY BA., MERRICK J.M.,
MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D.,
MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D.,
WEIDMAN J.E., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M.,
WHIDMAN J.E., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D.,
UTTERBACK T.K., HANNA M.C., NGUYEN D.T., SADUEK D.M., BRANDON R.C.,
FINE L.D., FRIFCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M.,
GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
11-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43)
(LECITHIN-CHOLESTEROL ACYLTRANSFERASE) (PHOSPHOLIPID-CHOLESTEROL ACYLTRANSFERASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAPIO ANUBIS (OLIVE BABOON).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Length 438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Indels
                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VENTER J.C.;
SCIENCE 269:496-512(1995).
-- SIMILARITY: STRONG, TO E.COLI YCEC.
-- SIMILARITY: BELONG; TO THE YABO/YCEC/SFHB FAMILY.
EMBL; U32724; G1573385; --
PROSITE; PS01129; YABO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 1.90e+00;
12; Mismatches 11
                           . 1.03e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               322 AA; 36588 MW; AD948C64 CRC32;
  DB 1;
                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                Ä
                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40 RLYELLHGAGNHAAGILTLGKRRPGPPGLQGRLQ 73
                                                                                                                                                                                                                                                                             322
  Score 88;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (REL. 32, LAST A
HYPOTHETICAL PROTEIN HI0412.
Query Match 9.8%;
Best Local Similarity 75.0%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 32.48;
les 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                            7 PWQRVLLLLGLLLPPA 22
                                                                                                                                           2 PWAAVTLLLLLLPPA 17
                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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MEDLINE; 95350630.
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Search completed: Thu Jul 30 09:27:36 1998 Job time: 11 secs.
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BIOCHEMISTRY 27:8443-8448(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BOS TAURUS (BOVINE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; ARTIODACIYLA.
                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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MEDLINE: 90256825.
YAMARAWA M., TANAKA M., KOYAWA M., KAGESATO Y., WATAHIKI M.,
TANAKHOTO M., NAKASHIMA K.;
J. BIOL. CHEM. 265:8915-8920(1990).
                                                                                                                                                                                   Length 1663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 236;
                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37 V -> A (IN REF. 2).
94 V -> F (IN REF. 2 AND 3).
170 V -> M (IN G163281).
26908 MW; 88029761 CRC32;
                                                                                                                 LK -> KL (IN REF. 2).
W; 0428CF63 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLACENTAL LACTOGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 85; DB 1; L
Pred. No. 2.57e+00;
                                                                                                                                                                                   Score 86; DB 1; L
Pred. No. 1.90e+00;
5; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-1989 (REL. 10, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
11-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
PLACENTAL LACTOGEN I PRECURSOR (BPLP-I).
                                                                                                                                                                                                                                                                                                                                                                                                                      236 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
BY SIMILARITY.
PROBABLE.
  BY SIMILARITY
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. MEDLINE: 89207456.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00266; SOMATOTROPIN_1; 1.
PROSITE; PS00338; SOMATOTROPIN_2; 1.
HORMONE; PLACENTA; GLYCOPROTEIN; SIGNAL.
                                                                  PROBABLE. PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                 722 LK
186460 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G163277; JOINED. G163277; JOINED.
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Best Local Similarity 38.2%;
Matches 13; Conservative
                                                                                                                                                                                   Query Match 9.6%;
Best Local Similarity 66.7%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                       |:||||||:::||:||
8 LLLLLLPPALLSIG 22
                                                                                                                                                                                                                                                                             10 LVLLLLLASSLLALG 24
                                                                    939
                                                                                                                                      1663 AA;
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    1518
1537
1010
939
1617
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ID PLC1_BOVIN
AC P09611;
                                                                    CARBOHYD
CARBOHYD
CONFLICT
SEQUENCE
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STEATINED 10;
MEDLINE; 93144351.
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MEDLINE; 93144351.
MEDLINE; 9314351.
MEDLINE; PELLER G., GERDAY C.;
BIOCHIM. BIOPHYS. ACTA 1171:331-333(1993).
II FUNCTION: CATALYZES LIPOLYSIS AT TEMPERATURES AS LOW AS 3 DEGREES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CELSIUS.
-1-CATALYTIC ACTIVITY: TRIACYLGIVCEROL + H(2)O = DIACYLGIVCEROL + A FAITY ACTOR ANION.
EMBL: X67712; G74786; -
PIR: S26486; S26486
PIR: S286486; S286486
PIR: S286120; LIPASE_SER; FALSE_NEG.
HYDROLASE; LIPID DEGRADATION; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
LIPASE 1.
POTENTIAL.
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                     PSYCHROBACTER IMMOBILIS.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; AEROBIC RODS AND COCCI;
NEISSERIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                    LIP1_PSYIM STANDARD; PRT; 317 AA.

002104;
01-01-1933 (REL. 26, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
LIPASE 1 PRECURSOR (EC 3.1.1.3) (TRIACYLGLYCEROL LIPASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 9.5%; Score 85; DB 1; Length 317; Best Local Similarity 35.1%; Pred. No. 2.57e+00; Matches 13; Conservative 9; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95 LIIPDLLGFGESSKPMSADYRSEAQRTRLHELLQAKG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 LLLLLVVSNLLLCQGVEDYA-P-YCKNQPGNCRI 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 317 AA; 35251 MW;
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ACT_SITE
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu Jul 30 09:26:50 1998; MasPar time 7.38 Seconds 608.699 Million cell updates/sec lar output not generated. :uo

>US-08-938-548A-10 (1-123) from US08938548A.pep 899 Description: Perfect Score:

1 VPWAAVTLLLLLLLPPALLS......GRGCPTVTTTALAPRGGSGV 123 Sequence:

PAM 150 Gap 11 Scoring table:

120441 segs, 36531193 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

pir56 Database:

Mean 39.443; Variance 86.453; scale 0.456 Statistics:

1:pirl 2:pir2 3:pir3 4:pir4 5:nrl3d

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	٠	æ					
Score		Query	Length	DB	a	Description	Pred. No.
101		11.2	131	-	SEPG	secretin precursor -	9.71e-02
86		10.9	641	~	A45054	probable intercellula	2.32e-01
96		10.7	601	7	B36346	fibulin 1 precursor,	4.12e-01
96		10.7	683	7	C36346	fibulin 1 precursor,	4.12e-01
92		10.2	838	~	145557	eyeless, long form -	1.27e+00
91		10.1	440	Н	XXHON	phosphatidylcholine	1.68e+00
91		10.1	602	7	S39782	cyclooxygenase 1 - ra	1.68e+00
8		9.9	602	~	S69198	prostaglandin G/H syn	2.91e+00
8		9.9	1061	Н	OYHUAR	natriuretic peptide r	2.91e+00
88		9.8	245	~	S43293	FLT3/FLK2 ligand (clo	3.81e+00
88		9.8	438	Н	XXMSN	phosphatidylcholine	3.81e+00
88		9.8	491	~	JC6197	stromelysin 3 (EC 3.4	3.81e+00
87		7.6	583	~	I50518	DNA binding protein E	4.99e+00
87		7.6	599	~	A36746	prostaglandin-endoper	4.99e+00
86		9.6	322	~	G64151	hypothetical protein	6.52e+00
98		9.6	410	~	S74705	hypothetical protein	6.52e+00
86		9.6	440	~	JC1502	phosphatidylcholine	6.52e+00
98		9.6	497	7	S43745	phosphatidylinositol-	6.52e+00
86		9.6	1663		C3RT	complement C3 precurs	6.52e+00
82		9.5	236	~	A37930	placental lactogen pr	8.50e+00
82		9.5	317	~	528225	triacylglycerol lipas	8.50e+00
82		9.5	317	7	S57275		8.50e+00
82		9.5	334	7	S16296	ferric enterobactin t	8.50e+00

#authors Gafvelin, G.; Joernvall, H.; Mutt, V.
#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:6781-6785
#title Processing of prosecretin: isolation of a secretin precursor from porcine intestine.
#cross-references MUID:90370867
#accession A36052

A90916

REFERENCE

tryptic peptides were sequenced A36052

##note

REFERENCE

#superfamily glucagon
amidated carboxyl end; duodenal mucosa; duplication; hormone;

CLASSIFICATION KEYWORDS

synthesis confirmed the proposed structure of the natural hormone

annotation

#contents #journal #title #authors

#note

Bodanszky, M.; Ondetti, M.A.; Levine, S.D.; Narayanan, V.L.; Saltza, M.V.; Sheehan, J.T.; Williams, N.J.; Sabo, E.F. Chem. Ind. (1966) :1757-1758
Synthesis of a heptacosapeptide amide with the hormonal activity of secretin.

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#description
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25-440
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                                                                                                                                                                                                                                                               FlyBase:ey
##cross-references FlyBase:EBgn0005558
itrons 37/1; 92/2; 152/3; 371/1; 429/1; 521/1; 639/2

FICATION #superfamily unassigned homeobox proteins; homeobox homology;
paired box homology
alternative splicing; DNA binding; homeobox; nucleus;
transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rogne, S.; Skretting, G.; Larsen, F.; Myklebost, O.; Mevag, B.; Carlson, L.A.; Holmquist, L.; Gjone, E.; Prydz, H. Blochem Blophys. Res. Commun. (1987) 148:161-169
The isolation and characterisation of a cDNA clone for human lecithin:cholesterol acyl transferase and its use to analyse the genes in patients with LCAT deficiency and fish
#authors Quiring, R.; Walldorf, U.; Kloter, U.; Gehring, W.J.
#journal Science (1994) 265:785-789
#title Homology of the eyeless gene of Drosophila to the Small eye
gene in mice and Aniridia in humans [see comments].
#cross-references MUID:94323757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   XXHUN #type complete
phosphatidylcholine--sterol O-acyltransferase (EC 2.3.1.43)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        McLean, J.; Fielding, C.; Drayna, D.; Dieplinger, H.; Baer, B.; Kohr, W.; Henzel, W.; Lawn, R. Proc. Natl. Acad. Sci. U.S.A. (1986) 83:2335-2339 Cloning and expression of human lecithin-cholesterol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #authors McLean, J.; Wion, K.; Drayna, D.; Fielding, C.; Lawn, R. #journal Nucleic Acids Res. (1986) 14:9397-9406
#title Human lecithin-cholesterol acyltransferase gene: complete gene sequence and sites of expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lecthin-choletterol acyltransferase precursor;
phospholipid--cholesterol acyltransferase precursor
#formal_name Homo sapiens #common_name man
04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A00571; A25575; A29661; JQ0036; A29133; I52260; A28511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #domain homeobox homology #label HOX
#length 838 #molecular-weight 87662 #checksum 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    681 PPPMAPAHHHIVPGDGGRPAGV-GLGSGQSANLGA-SCSGSGYEVLSAYALPP 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                     ##cross-references EMBL:X79493; NID:g641809; PID:g641810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 10.2%; Score 92; DB 2; Length 838; Best Local Similarity 28.3%; Pred. No. 1.27e+00; Matches 15; Conservative 19; Mismatches 17; Indels
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##residues 1-440 ##label MCL1
##cross-references GB:Ml2625; NID:9187022; PID:9307117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##residues 1-440 ##label MCL2
##cross-references GB:X04981; NID:g34286; PID:g34287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acyltransferase cDNA.
#cross-references MUID:86205950
#accession A00571
                                                                                                                                               ##status preliminary
##molecule_type mRNA
##residues 1-838 ##label RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 precursor - human
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Schindler, P.A.; Settineri, C.A.; Collet, X.; Fielding, C.J.; Sullingame, A.L.
Burlingame, A.L.
Protein Sci. (1995) 4:791-803
Site-specific detection and structural characterization of the glycosylation of human plasma proteins
lectinin:cholesterol acyltransferase and apolipoprotein D using HPLC/electrospray mass spectrometry and sequential glycosidase digestion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jr., A.M.; Pownall, H.J.
J. Biol. Chem. (1987) 262:3086-3091
Lecithin: cholesterol acyltransferase. Functional regions and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   catalyzes the transfer of sn-2 fatty acyl groups from phosphatidylcholine (lecithin) to sterol to form sterol fatty esters and 1-acylglycerphosphocholine palmitcyl, oleoyl, and linoleoyl residues can be transferred; a number of sterols, including cholesterol, can act as
                                                                                                                                                                                                                                                                                                              genomic clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yang, C.; Manoogian, D.; Pao, Q.; Lee, F.; Knapp, R.D.; Gotto
                                                                                                                                                                                                                                                                                                                                                                                                                                               ##molecule_type mRNA
##residues_17-256, H',258-440 ##label TAT
##cross-references GB.X06537; NID:934284; GB:M26268; NID:9187024;
##cross-references GB.X06537; NID:9187025
PID:9187025
##note the authors translated the codon CAT for residue 241 as
Ile and CAG for residues 251, 304, 368, 373, and 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #superfamily phosphatidylcholine--sterol acyltransferase
acyltransferase; cholesterol; glycoprotein; lipid metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bloch H.; Kusunoki, J.; Ogasawara, M.; Yamamoto, T.; Ohta, Y.; Shimada, T.; Saito, Y.; Yoshida, S.
Blochem. Blophys. Res. Commun. (1991) 181:93-940
Molecular defect in familial lecithin:cholesterol
acyltransferase (LOAP) deficiency: a single nucleotide
insertion in LCAT gene causes a complete deficient type of
                                                                                                                                                 Tata, F.; Chaves, M.E.; Markham, A.F.; Scrace, G.D.; Waterfield, M.D.; McIntyre, N.; Williamson, R.; Humphries,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ts annotation; peptide sequences; N- and O-glycosylation Apolipoprotein A-I (see PIR:LPHUA1) is a potent activator of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #domain signal sequence #status predicted #label SiG\
#product phosphatidylcholine--sterol acyltransferase
                                                                                                                                                                                                                                                           Biochim. Biophys. Acta (1987) 910:142-148
The isolation and characterisation of cDNA and ge
for human lecithin:cholesterol acyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##molecule_type protein
##residues 25-284,'Q',286-333,'Q',335-440 ##label YAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##residues 25-34,'AHHAQG' ##label BUJ ##cross-references GB:S74079; NID:g241428; PID:g241429 ##note defective frame shift mutant sequence
                                                                      ##cross-references GB:M17959; NID:g187026; PID:g386858
NCE A90666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a structural model of the enzyme.
#cross-references MUID:87137578
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#map_position 16q22.1-16q22.1
##molecule_type mRNA
##residues 13-440 ##label ROG
                                                                                                                                                                                                                                                                                                                                                                                *cross-references MUID:88050946
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#accession I52260
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I50518; S49141
I50518
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REFERENCE
#authors
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ORGANISM
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COMMENT
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Zurawski, S.; Bazan, J.F.; Kastelein, R.; Hudak, S.;
Wagner, J.; Mattson, J.; Luh, J.; Duda, G.; Martina, N.;
Peterson, D.; Menon, S.; Shanafelt, A.; Muench, M.; Kelner,
G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik,
A.; Rosnet, O.; Dubreuil, P.; Birnbaum, D.; Lee, F.
Injand for FLIJ*K2 receptor tyrosine kinase regulates
growth of haematopoietic stem cells and is encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #authors Warden, C.H.; Langner, C.A.; Gordon, J.I.; Taylor, B.A.;

#journal J. Biol. Chem. (1989) 264:21573-21581

#title Tissue-specific expression, developmental regulation, and chromosomal mapping of the lecithin:cholesterol acyltransferase gene. Evidence for expression in brain and testes as well as liver.

#cross-references MUID:90094326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1-245 ##label HAN
the authors translated the codon AGT for residue 25 as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      XXMSN #type complete
phosphatidylcholine--sterol O-acyltransferase (EC 2.3.1.43)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, July 1990
Promoter and 5' flanking sequences of the mouse LCAT gene. S21370
                                                                                                $43293  #type complete

FLT3/FLK2 ligand (clone $109) - human

#formal_name Homo sapiens #common_name man

20-oct-1994 #sequence_revision 10-Nov-1995 #text_change

10-Nov-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phospholipid-cholesterol acyltransferase precursor;
#formal_name Mus musculus #common_name house mouse
30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #length 245 #molecular-weight 27404 #checksum 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               precursor - mouse
lecithin--cholesterol acyltransferase precursor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 9.8%; Score 88; DB 2; Length 245; Best Local Similarity 50.0%; Pred. No. 3.81e+00; Matches 10; Conservative 8; Mismatches 1; Indels
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35
                                      8 LLLLLLPPALLSL-GVDAQPL 28
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14 LLLLLLPPLLLLLRGSHAGNL
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##residues 1-24:
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##cross-references EMBL:X54095; NID:952873; PID:952874

The active enzyme catalyzes the transfer of acyl groups from lecithin to sterol to form sterol esters. Palmitcyl, oleoyl, and linoleoyl residues can be transferred; a number of sterols, including cholesterol, can act as acceptor. Apolipoprotein A-I is a potent activator for this enzyme.

EICATION #superfamily phosphatidylcholine--sterol acyltransferase
                                                                                                                                                                                                                          acyltransferase; glycoprotein; lipid metabolism; lipoprotein
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##cross-references GB:U46034

This protein is a member of the matrix metalloproteinase family.
FICATION #superfamily interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase homology homology matrix metalloproteinase homology hydrolase; metalloproteinase; zinc; zymogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #domain matrix metalloproteinase homology #label MMP\
#domain hemopexin repeat homology #label PXN\
#binding_site zinc, catalytic (Cys, His, His, His)
(inhibited) #status predicted\
#binding_site zinc, catalytic (His) (active) #status
                                                                                                                                                                                                                                                                                          #domain signal sequence #status predicted #label SIG\
                                                                                                                                                                                                                                                                                                                       #product phosphatidylcholine--sterol acyltransferase
#status predicted #label MAT\
#binding_site carbohydrate (Asn) (covalent) #status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISO518 #type complete
DNA binding protein E12 - zebra fish
#formal_name Brachydanio rerio #common_name zebra fish
13-5ep-1996 #sequence_revision 13-5ep-1996 #text_change
16-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JC6197 #type complete
stromelysin 3 (EC 3.4.24..) - rat
#formal_name Rattus norvegicus #common_name Norway rat
11-Apr-1997 #sequence_revision 09-May-1997 #text_change
20-Mar-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Okada, A.; Saez, S.; Misumi, Y.; Basset, P.
Gene (1997) 185:187-193
Rat stromelysin 3: CDNA cloning from healing skin wound,
activation by furin and expression in rat tissues.
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Pred. No. 3.81e+00;
16; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 88; DB 1; Length 438; Pred. No. 3.81e+00;
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#length 491 #molecular-weight 55511 #
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#length 438 #mol
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Best Local Similarity 35.0%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 75.0%;
Matches 12; Conservative
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Thu Jul 30 09:26:03 1998; MasPar time 5.63 Seconds 335.050 Million cell updates/sec Run on:

>US-08-938-548A-10 (1-123) from USO8938548A.pep 899 1 VPWAAVTLLLLLLPPALLS......GRGCPTVTTALAPRGGSGV 123 ular output not generated.

Title: Description: Perfect Score: Sequence:

124785 seqs, 15338987 residues PAM 150 Gap 11 Scoring table: Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

a-geneseq31-2
l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
l:part1 2:part9 10:part10 11:part11 12:part13 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 Database:

Mean 29.422; Variance 127.873; scale 0.230 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Core Augraph DB ID Description Pre- 1 96 10.7 566 2 R11148 Fibulin A. 5.11 2 5 10.7 603 2 R11149 Fibulin B. 5.11 3 96 10.7 603 2 R11150 Fibulin C. 5.11 4 0 2 R24189 Human d-IBB-L Polypep 1.2 8 9 8 254 12 R64190 Human d-IBB-L Polypep 2.0 8 9 8 254 25 W26657 Human d-IBB-L Polypep 2.0 8 9 8 254 25 W26657 Human d-IBB-L Polypep 2.0 9 87 9.7 111 7 R35515 Tryptophan aporepress 2.3 10 85 9.5 363 23 W12414 Porcine Complement in 3.3 11 84 9.3 234 16 R82605 Fibulin Candplement in 3.9 12 84 9.3 238 13 R71481 Human R86/5109 Fils 4.6 16 83 9.2 235 13 R66175 Human R86/5109 Fils 4.6 19 83 9.2 235 12 R67541 Human R1-3 Japand. 4.6 19 83 9.2 235 R80049 ICP34.5 Fagment. 4.6 10 10 10 10 10 10 11 12 10 10 10 12 13 13 10 10 10 13 14 15 10 10 14 15 13 10 10 15 16 17 10 10 16 17 10 10 17 18 10 10 18 18 10 10 19 10 10 10 10 10 10 10 11 10 10	1					SUMMARIES		
96 10.7 566 2 R11148 Fibulin A. 96 10.7 601 2 R11149 Fibulin B. 96 10.7 683 2 R11150 Fibulin C. 91 10.1 440 25 W24789 Human lecithin-choles I 10.1 440 25 W24789 Human lecithin-choles I 88 9.8 254 12 R64190 Human 4-1BB-L polypep 2 88 9.8 254 25 W26657 Human 4-1BB-L polypep 2 87 9.7 599 4 R21690 Prostaglandin endoper 2 85 9.5 363 23 W14414 Porcine complement in 3 84 9.3 234 16 R82065 Eph transmembrane tyr 8 9.3 1239 R4481 Glutamin exid recepto 3 83 9.2 235 13 R66175 Human S86/S109 Flt3 1 4 8 9.2 235 13 R65751 Human S86/S109 Flt3 1 4 8 9.2 235 13 R65751 Human S86/S109 Flt3 1 4 8 9.2 235 13 R65751 Human S86/S109 Flt3 1 4 8 9.2 235 12 R67541 Human Flt-3 ligand.	Result No.	Score	% Query Match	Length	DB	A	Description	Pred. No.
96 10.7 601 2 R11149 Fibulin B. 95 10.7 683 2 R11150 Fibulin C. 99 10.1 440 2 P70134 Buman lecithin-choles 1. 91 10.1 440 25 W24789 Buman lecithin-choles 1. 91 10.1 440 25 W24789 Buman 4-1BB-L polypep 2. 88 9.8 254 12 R64190 Buman 4-1BB-L polypep 2. 87 9.7 11 7 R35515 Frogham aporepres 2. 87 9.7 599 4 R21690 Prostaglandin endoper 2. 85 9.5 363 23 W12414 Porchae Complement in 3. 84 9.3 234 16 R82605 Eph transmembrane tyr 3. 1239 9 R459456 Glutanic acid recepto 3. 84 9.3 1239 9 R45945 Glutanic acid recepto 3. 88 9.2 235 13 R66175 Buman S86/S109 Flt3 1 4. 83 9.2 235 12 R65741 Buman flt-3 ligand. 4 83 9.2 252 4 R21708 Buman flt-3 ligand. 4 83 9.2 252 8 R50049 ICP34.5 fraqment.	٦	96	10.7	266	7	R11148	Fibulin A.	5.13e+00
96 10.7 683 2 R11150 Fibulin C. 91 10.1 440 2 P70134 Natural recombinant h 1. 91 10.1 440 25 W24789 Natural recombinant h 1. 91 10.1 440 25 W24789 Natural recombinant h 1. 91 10.1 440 25 W24789 Natural recombinant h 1. 91 10.1 440 25 W2657 Human 4-IBB-L polypep 2.0 88 9.8 254 12 W2657 Human 4-IBB-L polypep 2.0 87 9.7 131 R35515 Tryptophan aporepress 2. 85 9.5 363 23 W12414 Protein ecomplement in 3. 84 9.3 23 W12414 Protein ecomplement in 3. 84 9.3 238 13 R71481 Human hek-L protein for 3. 84 9.3 1239 9 R45945 Glutamic acid recepto 3. 83 9.2 235 13 R66175 Human S86/S109 Fit3 1 4. 83 9.2 235 12 R65741 Human flt-3 ligand, 4. 83 9.2 252 4 R21708 Human flt-3 ligand, 4. 83 9.2 258 8 R50049 ICP34.5 fragment.	7	96	10.7	601	N	R11149	Fibulin B.	5.13e+00
91 10.1 440 2 P70134 Natural recombinant h 1 91 10.1 440 25 W24789 Human lecithin-choles 1 91 10.1 440 25 W24789 Human 4-LBB-L p-Optyee 1 88 9.8 254 25 W26657 Human 4-LBB-L p-Optyee 2 87 9.7 111 7 R35515 Tryptophan aporepress 2 85 9.5 363 23 W12414 Porcine complement in 3 84 9.3 23 W12414 Porcine complement in 3 84 9.3 238 13 R71481 Human hek-L protein f 3 84 9.3 1239 9 R45945 Glutamic acid recepto 3 84 9.3 1239 9 R45945 Glutamic acid recepto 3 83 9.2 235 13 R66175 Human flt-3 ligand. 83 9.2 235 13 R66175 Human flt-3 ligand. 83 9.2 252 4 R21708 Hyp. 10794.5 fragment. 83 9.2 258 R50049 ICP44.5 fragment.	m	96	10.7	683	N	R11150	Fibulin C.	5.13e+00
91 10.1 440 25 W24789 Human lecithin-choles 1 88 9.8 254 12 R64190 Human 4-1BB-1 polypep 2 88 9.8 254 12 R64190 Human 4-1BB 11gand. 2 87 9.7 111 7 R35515 Human 4-1BB 11gand. 2 87 9.7 111 7 R35515 Tryptophan aporepress 2 85 9.5 363 3 W12414 Porcine complement in 3 84 9.3 234 16 R82605 Eph transmembrane tyr 3 84 9.3 123 9 R45945 Glutamic acid recepto 3 84 9.3 1239 9 R45945 Glutamic acid recepto 3 83 9.2 235 13 R65175 Human S86/S109 Flt3 1 4 83 9.2 235 14 R67541 Human S86/S109 Flt3 1 4 83 9.2 258 R50069 ICP34.5 fragment. 4 84 9.3 129 R65056 ICP34.5 fragment. 4 85 9.2 258 R50069 ICP34.5 fragment. 4 86 9.2 258 R50069 ICP34.5 fragment. 4	7	91	10.1	440	~	P70134	Natural recombinant h	1.21e+01
88 9.8 254 12 R64190 Human 4-1BB-L polypep 2 824 25 W26557 Human 4-1BB-L polypep 2 9.7 599 4 R21690 Prostaglandin endoper 2 85 9.5 363 23 W14414 Porcine complement in 3 84 9.3 234 16 R8265 Eph transmembrane tyr 3 84 9.3 238 13 R71481 Human hek-L protein. 3 84 9.3 1239 9 R45045 Glutamic acid recepto 3 83 9.2 235 13 R66175 Human S86/2109 F1t3 1 4 83 9.2 235 12 R67541 Human S86/2109 F1t3 1 4 83 9.2 258 8 R50049 ICP34.5 fragment.	'n	91	10.1	440	25	W24789	Human lecithin-choles	1.21e+01
88 9.8 254 25 W26657 Human 4-1BB ligand. 2 87 9.7 111 7 R35515 Tryptophan aporepress 2 87 9.7 111 7 R35515 Tryptophan aporepress 2 88 9.5 363 23 W12414 Proctane complement in 3 84 9.3 35 1 P94256 Truncated E protein fi 3 84 9.3 234 16 R82605 Eph transmembrane tyr 3 84 9.3 1239 9 R45945 Glutamin hek-L protein. 3 84 9.3 1239 9 R45945 Glutamin cacid recepto 3 83 9.2 235 13 R66175 Human S86/2109 Flt3 1 83 9.2 235 12 R67541 Human flt-3 ligand. 4 83 9.2 258 8 R50049 ICP34.5 fragment. 4 83 9.2 258 R50049 ICP34.5 fragment. 4 83 9.2 258 R50049 ICP34.5 fragment. 4	9	88	9.8	254	12	R64190	Human 4-1BB-L polypep	2.01e+01
87 9.7 111 7 R35515 Tryptophan aporepress 2 87 9.7 599 4 R21690 Prostaglandin endoper 2 85 9.3 38 11 P94256 Truncated E protein 1 3 84 9.3 234 16 R82665 Eph transmembrane tyr 3 84 9.3 234 18 R82665 Eph transmembrane tyr 3 84 9.3 238 13 R71481 Human hek-L protein. 3 84 9.2 235 13 R6175 Human S86/S109 Flt3 1 4 83 9.2 235 13 R65741 Human S86/S109 Flt3 1 4 83 9.2 235 14 R21708 Howan flt-3 ligand. 4 83 9.2 258 8 R50049 ICP34.5 fragment.	7	88	9.8	254	52	W26657	Human 4-1BB liqand.	2.01e+01
87 9.7 599 4 R21690 ProstaglandIn endoper 2 85 9.5 363 23 Wildlife Profile Complement in 3 84 9.3 234 16 R8265 Eph transmembrane tyr 3 84 9.3 234 16 R8265 Eph transmembrane tyr 3 84 9.3 1239 9 R45945 Glutamic acid recepto 3 83 9.2 235 13 R6175 Human R64/2109 Flt3 1 4 83 9.2 235 13 R65754 Human S86/S109 Flt3 1 4 83 9.2 255 4 R21708 HSV-1 (CVG-2) icpat. 5 fragment.	ω	87	9.7	111	7	R35515	Tryptophan aporepress	2.38e+01
85 9.5 363 23 W12414 Porcine complement in 3 84 9.3 35 1 P94256 Truncated E protein f 3 84 9.3 234 16 R82565 Eph transmembrane tyr 3 84 9.3 1239 9 R45945 Glutamic acid recepto 3 83 9.2 179 8 R50056 ICP34.5 fragment 4 83 9.2 235 13 R66175 Human S86/5109 Flts 1 4 83 9.2 255 4 R21708 HSV-1 (CVG-2) ICP34.5 4 83 9.2 258 8 R50049 ICP34.5 fragment 4 83 9.2 258 8 R50049 ICP34.5 fragment 4 8 83 9.2 258 8 R50049 ICP34.5 fragment 4 8 8 9.2 258 R50049 ICP34.5 fragment 4 8 8 9.2 258 R50049 ICP34.5 fragment 4 8 9 9.2 258 R50049 ICP34.5 fragment 4 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	σ	87	9.7	299	4	R21690	Prostaglandin endoper	2.38e+01
84 9.3 35 1 P94256 Truncated E protein f 3 84 9.3 234 16 R8265 Eph transmembrane tyr 3 84 9.3 238 13 R71481 Human hek-L protein. 3 84 9.3 1239 9 R45945 Glutamic acid recepto. 8 9.2 179 8 R50056 ICP34.5 fragment. 4 83 9.2 235 13 R66175 Human S86/S109 Flt3 1 4 83 9.2 235 14 R21708 Howan flt-3 ligand. 4 83 9.2 258 8 R50049 ICP34.5 fragment.	10	82	9.5	363	53	W12414	Porcine complement in	3.33e+01
84 9.3 234 16 R82605 Eph transmembrane tyr 3 84 9.3 238 13 R71481 Human hek-L protein. 3 84 9.3 1239 9 R45945 Glutamic acid recepto 3 83 9.2 179 8 R50056 ICP34.5 fragment. 4 83 9.2 235 13 R66175 Human S86/S109 Flt3 1 4 83 9.2 235 4 R21708 HSV-1 (CVG-2) ICP34.5 4 83 9.2 258 8 R50049 ICP34.5 fragment. 4 83 9.2 258 R50049 ICP34.5 fragment.	11	84	e. 6	35		P94256	Truncated E protein f	3.93e + 01
84 9.3 238 13 R71481 Human hek-L protein. 3 84 9.3 1239 9 R45945 Glutamin cacid recepto 3 83 9.2 179 8 R50056 ICP34.5 fragment. 83 9.2 235 13 R66175 Human S86/5109 Flt3 1 4 83 9.2 254 R21708 HSV-1 (CVG-2) ICP34.5 4 83 9.2 258 8 R50049 ICP34.5 fragment. 4 8 83 9.2 258 R50049 ICP34.5 fragment.	12	84	9.3	234	16	R82605	Eph transmembrane tyr	3.93e+01
84 9.3 1239 9 R45945 Glutamic acid recepto 3 83 9.2 179 8 R50056 ICP34.5 fragment. 4 83 9.2 235 13 R66175 Human S86/S109 Flt3 1 4 83 9.2 235 12 R67541 Human ILt-3 ligand. 4 83 9.2 252 4 R21708 HSV-1 (CVG-2) ICP34.5 fragment.	13	84	9.3	238	13	R71481	Human hek-L protein.	3.93e+01
83 9.2 179 8 R50056 ICP34.5 fragment. 4 83 9.2 235 13 R66175 Human S86/S109 Flt3 1 4 83 9.2 235 12 R67541 Human flt-3 ligand. 4 83 9.2 254 R21708 HSV-1 (CVG-2) ICP34.5 4 83 9.2 258 R50049 ICP34.5 fragment. 4	14	84	9.3	1239	σ	R45945	Glutamic acid recepto	3.93e+01
83 9.2 235 13 R66175 Human S86/S109 Flt3 1 4 83 9.2 235 12 R67541 Human flt-3 ligand. 4 83 9.2 252 4 R21708 HSV-1 (CVG-2) ICP94.5 4 83 9.2 258 R50049 ICP34.5 fragment. 4	15	83	9.5	179	œ	R50056	ICP34.5 fragment.	4.63e+01
83 9.2 235 12 R67541 Human flt-3 ligand. 4 83 9.2 252 4 R21708 HSV-1 (CVG-2) ICP34.5 4 83 9.2 258 8 R50049 ICP34.5 fragment. 4	16	83	9.5	235	13	R66175		4.63e+01
83 9.2 252 4 R21708 HSV-1 (CVG-2) ICP34.5 4 83 9.2 258 8 R50049 ICP34.5 fragment.	17	83	9.5	235	12	R67541	f1t-3	4.63e+01
8 R50049 ICP34.5 fragment. 4	18	83	9.5	252	4	R21708	(CVG-2)	4.63e+01
	19	83	9.5	258	ω	R50049	•	4.63e+01

ALIGNMENTS

l; Protein; 566 AA.	(first entrv)		1; adhesion; receptor; fibronectin.		Location/Qualifiers		/label= signal sequence	Jabel fibulin A		/label= N-linked glycosylation		/label= N-linked glycosylation 339	/label- N-linked glycosylation		/label= type I motif 3669	/label- repeat unit 1		/label= repeat unit 2	1441/9 /label= Glu/Asp-rich region	180566	/label type II motif	180214 /label= repeat unit 1		/label- consensus pentapeptide	4	/label= repeat unit 2 261265	/label= consensus pentapeptide		/label- repeat unit 3	/label= consensus pentapeptide		/label= repeat unit 4 355 350	
RESULT I ID R11148 standard;	R11148; 21-MAY-1991 (f		Beta-1 integrin;	^	Key	peptide		procein	modified_site		modified_site	modified site)	region	region		region		region	region	•	region	region		region	region	n	region		101601	region	40,100	
3 C	D PC	DE	ΚM	SO	ΗΉ	FT	H E	4 E4	H	FI	F	F.F.	FT	FI	F F	FT	F	E .	- E	F	E I	FF	Ë	F	E	E E	FI	FT	FF	H	F	H H	•

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the repeat lacking two Cys residues. The same motif is found in albumin, vitamin D-binding protein and alpha-fetoprotein. The albumin, vitamin D-binding protein and alpha-fetoprotein. The disulphide stabilized loop structure is thought to be conserved. The type II motif, related to repeats found in epidermal growth actor precursor is a 6-Cys pattern repeated nine times, although the ninth repeat in the A form is incomplete. Four of the repeats, (2, 3, 4 and 9) differ from the EGF-like motif in having a 4-6 consensus sequence for Asp and Ash hydroxylation. The 7th repeat consensus sequence for Asp and Ash hydroxylation. The 7th repeat consensus sequence ED/V/Cylation sequence, CXCXPC. Immediately following each repeat is a pentapeptide with the consensus sequence XD(I/V)(D/N)E. Fibulin binds to the cytoplasmic domain of the betal subunit of integrin adhesion receptors in a cation-dependent, EDFA-reversible manner. It can be used to manipulate adhesion of cells to fibronectin, collagen, with the protein have important diagnostic and therapeutic uses. Sequence 601 AA;
                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                           Length 601;
                                                                                                                                                                                                                                                                                                                                        8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Beta-1 integrin; adhesion; receptor; fibronectin.
Homo sapiens
                                                                                                                                                                                                                                                                                                             Score 96; DB 2; I
Pred. No. 5.13e+00;
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/label- consensus pentapeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1..29
/label- signal sequence
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/label= repeat unit 1
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/label= repeat unit 2
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/label= type II motif
180..214
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215..219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36.144
/label= type I motif
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/label- fibulin C
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R11150 standard; Protein; 683 AA.
                                                                                                                                                                                                                                                                                                             Query Match 10.7%;
Best Local Similarity 57.1%;
Matches 16; Conservative
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21-MAY-1991 (first entry)
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Purified fibulin, DNA encoding it and antibodies reactive with it useful as diagnostic and therapeutic component.

Useful as diagnostic and therapeutic component.

Claim 10, Fig 5: 56pp; English.

The fibulin A, B and C forms are identical from their N-terminals to a divergence point at posn. 566 (terminal codon in fibulin A) and stained; encoding polypeptides of 566, 601 and analysis with on and spacing of the Cys residues revealed two cys repeat moftif (I and II). The type I motif, CC(X)12C-(X)9-10C(X)6CC is repeated twice, separated by an imperfect form of the repeat lacking two Cys residues. The same motif is found in complement components C3a, C4a and C5s; the inverse is found in albumin, vitamin D-binding protein and alpha-fetoprotein. The disulphide-stabilized loop structure is thought to be conserved.

The type II motif, related to repeats found in epidermal growth factor precursor is a 6-Cys pattern repeated nine times, although the ninth repeat in the A form is incomplete. Four of the repeats (2, 3, 4 and 9) differ from the EGF-like motif in having a 4-6 consensus sequence for Asp and Asn hydroxylation. The 7th repeat consensus sequence for Asp and Asn hydroxylation. The 7th repeat consensus sequence XD(I/V)(D/N)E. Fibulin binds to the cytoplasmic domain of the betal subunit of integrin adhesion receptors in a cation-dependent, EDTA-reversible manner. It can be used to manipulate adhesion of cells to fibronectin, collagen, with the contents and cation-dependent, EDTA-reversible manner.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    laminin, and possibly also other proteins. Antibodies reactive with the protein have important diagnostic and therapeutic uses. See also R11147, R11148 and R11149.
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P70134 standard; Protein; 440 AA.
P70134;
26-APR-1991 (first entry)
Natural recombinant human lecithin:cholesterol acyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ü
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                                                                                                                                             440..444
/label= consensus pentapeptide
                                                                                                                                                                                                                                         consensus pentapeptide
                                                                                                                                                                                                                                                                                                                /label - consensus pentapeptide
               consensus pentapeptide
                                                                                        /label consensus pentapeptide
                                                   repeat unit 5
                                                                                                                            /label= repeat unit 6
                                                                                                                                                                                445..479
/label- repeat unit 7
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/label- repeat unit 8
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                                                                                                                                                                                                                                                                                                                                                                  17-AUG-1990; U04662.
18-AUG-1999; US-395773.
(LJOL-) LA JOLLA CANCER RES.
(AMNA-) AMER NAT RED CROSS.
RUOSIBILI EI, ARGRAVES WS;
WPI: 91-087250/12.
N-PSDB; Q11010.
                                                                                                         403..439
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                                360..397
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                                                                 23-JUL-1992
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Bourdon M, Lernhardt W, Youderlan P;

WADI: 93-036327044.

Tryptophan aporepressor used in vaccine prodn., etc. - contains

Within its' amino acid sequence, a peptide segment heterologous

to the aporepressor located on aq. solvent-assessible surface

Claim 4 + 20; Page 68 + 72; 82pp; English.

The hybrid protein contg. receptor binding sites is active as ligand

for mammalian cell receptors and can be used for a variety of

applications including treatment of diseases resulting from receptor/

ligand dysfunction, and in vaccine prodn.
                                                             The monoding 4-1BB ligand polypeptide(s) - useful for stimulating T-cell proliferation in vitro, and as research tools
This protein comprises human 4-1BB ligand (4-1BB-L), a novel
C-cytokine capable of binding cell surface receptor 4-1BB (see
C-comprise). Its amino acid sequence was deduced from an isolated
C-comprise and sequence was deduced from an isolated
C-comprise and acid sequence was deduced from an isolated
C-comprise and also been identified (see W26656). Human
4-1BB-L polypeptides, especially claimed soluble polypeptides
C-comprising the 4-1BB-L extracellular domain (amino acids 49-254),
C-can be expressed in transformed host cells. They can be used to
S-timulate T-cell proliferation in vitro, as research tools and as immunostimulants for purifying 4-1BB. They may also be useful as immunostimulants for therapeutic purposes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 lpllnlmltpderealgtrvriveecsrrgdmscsgrelknelgagiatitrgsnslkaa 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                             R35515 standard; protein; 111 AA.
R35515;
G9-5012-1993 (first entry)
Tryptophan aporepressor (2.7).
TA; N-terminal; C-terminal; tenascin; ligand; binding site;
                                                                                                                                                                                                                                                                                       Length 254;
                                                                                                                                                                                                                                                                                       Score 88; DB 25; Length 254
Pred. No. 2.01e+01;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 87; DB 7; Length 111;
Pred. No. 2.38e+01;
18; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61..69
/note= "tenascin ligand binding site"
70.111
/note= "TA C-terminal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1..60
/note- "TA N-terminal portion"
                           Smith CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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9.7%;
Best Local Similarity 27.6%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                       uery Match 9.8%;
Best Local Similarity 66.7%;
Matches 12; Conservative
                      Alderson MR, Goodwin RG, WPI; 97-502333/46.
N-PSDB; T91025.
                                                                                                                                                                                                                                                                                                                                             27 lpwalvaglillllaaa 44
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21-JUN-1991; US-720;
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            IMMA ) IMMONEX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
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Claim 3; Page 12-14; 20pp; Japanese.
This protein is a porcine complement inhibitor encoded by pMCPCDNA (TRIO98). The DNA is useful for large scale production of the forcembinant porcine complement inhibitor, which is useful for porcine organ transplantation into humans. The DNA clone pMCPcDNA is also useful in the analysis of the promoter region of porcine complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ï
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WPI: 97-08738,08.
N-PSDB; 761098.
N-Romerceding porcine complement inhibitor - useful in porcine organ
                                                                                                                                                                                                                                                                                                                                                                                                                                      antiinflammatory agents
Claim 1; Page 1; 10pp; Japanese.
The protein sequence of hPES was deduced from the CDNA sequence
obtd. by screening a human genomic library in EMBL3. hPES can be
used to screen anti-inflammatory agents. An anti-body against a
peptide specific to hPES can be made, and used for the determin-
ation of the protein.
Sequence 599 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ä
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porcine; pig; complement; inhibitor; organ transplantation; analysis; promoter.
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Pred. No. 3.33e+01;
10; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                prostaglandin endo-peroxide synthase - for screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 87; DB 4; Length 599;
Pred. No. 2.38e+01;
4; Mismatches 7; Indels
                                                                                                                                       Prostaglandin endoperoxide synthase.
Human; hPES; screening; anti-inflammatory; antibody.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 lillilippipviladpgaptpvnpcc 36
LT 9
R21690 standard; Protein; 599 AA.
R21690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W12414 standard; Protein; 363 AA.
W12414;
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                                                                                                                                                                                                                                               14-FEB-1992.
13-JUN-1990; 152784.
13-JUN-1990; JP-152784.
(MEIP ) MEIJI MILK PRODS KK.
WPI; 92-101937/13.
N-PSDB; Q23001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 9.7%;
Best Local Similarity 51.9%;
Matches 14; Conservative
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Best Local Similarity 34.3%;
Matches 12; Conservative
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                                                                                                           (first entry)
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19-JUN-1996; JO1704.
20-JUN-1995; JP-178254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transplant to humans
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DNA sequences of HSV-1 strains F (Q50037-38, Q50040-42), 17577+ (Q50043-45, Q58777), MGH-10 (Q58778-83), and CVG-2 (Q58784-88) and the predicted open reading frames for ICP34.5 (R50048-58) are compared in Fig 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pisclosure, Page 74-75, 95pp, English.

Programmed cell death may be treated through the use of the HSV-1 gene gammal 34.5 or prod. of its expression, ICP34.5. The gene and its expression have been demonstrated to be required for HSV-1 neurovirulence, and in partic., to act as an inhibitor of neuronal programmed cell death which allows for viral replication. Use of the gene therapy, or the protein itself, can be expected to result in inhibition of programmed cell death in various neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                       "This line is ommited in the specification"
                                 "This line is ommited in the specification"
                                                                                                           /note= "This line is ommited in the specification"
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WPI; 93-336453/42.
Use of gamma, 34.5 gene or encoded ICP 34.5 - for preventing or
treating programmed cell death in neuronal cells or in screening
                                                                                                                                                                                                                                                      New glutamic acid receptor and gene - for use in analysis of synaptic signal translation, and diagnosis of brain disease claim 1; Page 25-31; 35pp; Japanese.
The sequence shows a glutamic acid receptor. The receptor is useful for the analysis of nerve signal translation; within the synapse, expresssion of synapse plasticity, nerve cell necrosis, brain structure and brain disease. It can also be used in gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1239;
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Pred. No. 3.93e+01;
8; Mismatches 15; Indels
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Pred. No. 4.63e+01;
13; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gammal 34.5; ICP34.5; programmed cell death; apoptosis; neurovirulence; inhibition; viral replication; gene the neurodegenerative disease; herpes simplex virus; ss.
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Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R50056 standard; Protein; 179 AA
                                                                                                                                                                                30-JUN-1992; JP-173155.
(MITU ) MITSUBISHI KASEI CORP.
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Best Local Similarity 32.8%;
Matches 19; Conservative
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Local Similarity 38.5%;
les 15; Conservative
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04-MAY-1994 (first entry)
                                                                       /note= "T
883..891
                                                      ..630
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31-MAR-1992; US-861233.
(ARCH-) ARCH DEV CORP.
Chou J, Roizman B;
                                   /note=
622..6
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                                                                                                                            J06014783-A
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61 RRPGPP-GLQGRLQRLLQANGNHAAGILTMGRRAGAELEPHPCSGRGCPTVTTTALAP 117
                                                                         Search completed: Thu Jul 30 09:26:32 1998 Job time: 29 secs.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Thu Jul 30 09:28:36 1998; MasPar time 1.82 Seconds 395.942 Million cell updates/sec Run on:

>US-08-938-548A-10 (1-123) from USO8938548A.pep 899 1 VPWAAVTLLLLLLPPALLS......GRGCPTVTTTALAPRGGSGV 123 ular output not generated. Title:

Description: Perfect Score: Sequence:

63816 seqs, 5850866 residues PAM 150 Gap 11 Searched:

Scoring table:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Mean 27.378; Variance 125.728; scale 0.218 a-issued 1:5_COMB 2:PCT9_COMB 3:backfiles Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query	Query Match Length DB	DB	a	Description	Pred. No.
1	88	9.6	254	П	US-08-236-	Sequence 4, Applicatio	8.21e+00
7	84	9.3	238	-	US-08-453-	7	1.58e+01
m	84	6.6	238	-	US-08-240-	7	1.58e+01
4	84	9.3	1239	٦	US-08-026-	'n	1.58e+01
ß	83	9.5	235	N	PCT-US94-0	9	1.86e+01
	83	9.5	235	ч	US-08-243-	9	1.86e+01
7	83	9.5	263	~	PCI-US91-0	7	1.86e+01
ω	82	9.1	220	m	5175255-4	Patent No. 5175255.	2.18e+01
σ	81	9.0	226	m	5498600-2	Patent No. 5498600.	2.56e+01
10	81	0.6	241	m	5175255-8	Patent No. 5175255.	2.56e+01
11	81	0.6	241	m	5175255-2	Patent No. 5175255.	2.56e+01
12	81	9.0	282	1	US-08-445-	Sequence 1, Applicatio	2.56e+01
13	80		492	•	US-08-001-	4,	3.01e+01
14	80	8.9	492		US-07-794-	4	3.01e+01
15	80	8.9	1337	7	PCT-US95-0	7	3.01e+01
16	79	8.8	241	m	5194596-15	Patent No. 5194596.	3.53e+01
17	79	8.8	241	-	US-08-387-	Sequence 4, Applicatio	3.53e+01
18	79	8.8	241	7	PCT-US96-0	6	3.53e+01
19	78	8.7	555	7	US-08-484-	ý	4.14e+01
20	78	8.7	1184	ч	US-08-446-	Sequence 20, Applicati	4.14e+01
21	78	8.7	1184	Н	US-08-446-	20,	4.14e+01
22	78	8.7	1187	-	OS-08-097-	13,	4.14e+01
23	78	8.7	1187	Н	US-08-357-	Sequence 8, Applicatio	4.14e+01

4. 856+01 4. 856+01 4. 856+01 4. 856+01 5. 676+01 5. 676+01 5. 676+01 5. 676+01 5. 676+01 5. 676+01 6. 646+01 6. 646+01					
Sequence 8, Applicatio Sequence 2, Applicatio Sequence 2, Applicatio Sequence 10, Applicatio Sequence 10, Applicatio Sequence 36, Applicatio Sequence 2, Applicatio Sequence 3, Applicatio Sequence 11, Applicatio Sequence 3, Applicatio Sequence 3, Applicatio Sequence 3, Applicatio Sequence 3, Applicatio Sequence 5, Applic		254 AA.			nated 4-1BB Ligand Immunex Corporation n #6.0.1 8A
PCT - US95 - 1 SP PCT - US91 - 0 SP PCT - US91 - 0 SP PCT - US91 - 0 SP PCT - US94 - 0 SP PCT - US94 - 0 SP PCT - US95 - 0 SP PCT - US96 -	ALIGNMENTS	ARD; PRI;		US/08236918A	### ### ### ### ### ### ### ### ### ##
1187 589 2 589 2 589 1 2 519 1 2 250 3 2 250 3 2 250 3 2 250 3 2 250 3 2 250 3 2 2 3 2 2 3 2 2 3 2 2 3 2 3 3 3 3 4 4 8 8 3 5 5 8 5 3 5 8 5 3 6 8 9 3 3 7 8 9 8 9 3 3 8 9		STANDARD;		Application US	Sequence 4, Application US/082369 Patent No. 5674704 GENERAL INFORMATION: APPLICANT: Alderson, Mark R. APPLICANT: Godwin, Raymond GAPLICANT: Godwin, Raymond GAPLICANT: Smith, Craig A. TITLE OF INVENTION: Cytokine NUMBER OF SEQUENCES: 18 CORRESPONDENCE ADDRESS: ADDRESSEE: Rathryn A. Ander STREET: 51 University Stree CITY: Seattle STREET: 51 University Stree STREET: 910 University Stree COUNTRY: US ZIP: 98101 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: Apple Power Macin OPERATING SYSTEM: Apple 7.5 SOFTWARE: MACTOSOft Word, VCURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/2 FILING DATE: 06-May-1994 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: AADDRESSIFICATION: A35 ATTORNEY/AGENT INFORMATION: REFERENCE/DOCKET NUMBER: 28 TELEPHONE: A050 587-0430 TELEPHONE: (206) 533-0644 INFORMATION FOR SED ID NO: 4: ELEPHONE: 254 mmino acids
$\begin{array}{c} \alpha \alpha$		-918A-4		4, Appl:	dequence 4, Applicat atent No. 5674704 GENERAL INFORMATION APPLICANT: ALGEN APPLICANT: GOOWN APPLICANT: Smith TITLE OF INVENTION NUMBER OF SEQUENC CORRESPONDENCE ADDRESSE: Xat. STREET: 51 Univ. STREET: 51 Univ. STREET: 51 Uni. STREET: 52
5 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		T US-08-236	XXXXX	Seguence	Sequence 4, Patent No. 5 GENERAL INE APPLICAMY APPLICAMY APPLICAMY TITLE OF NUMBESS STREET: CITY: CITY: COMPUTER MEDIUM COMPUTER APPLICA APPLICA APPLICA APPLICA TILING CLASSIE FILING CLASSIE FILING CLASSIE FILING TILING
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Sequence 3, Application US/08026138E
Patent No. 5502166
GENERAL INFORMATION:
APPLICANT: Masayoshi MISHINA
TITLE OF INVENTION:
NUMBER O ESQUENCES: 19
CORRESPONDENCE ADDIABATE RESIDENCE 1-107
STREET: 5214, Nishiohata Residence 1-107
COMPUTR: Unigata-Ken
COMPUTR: JAPAN
ZIP: 951
COMPUTR: DISKette, 3.50 inch, 1.44 MB storage
COMPUTR: DISKette, 3.50 inch, 1.44 MB storage
COMPUTR: DISKette, 3.50 inch, 1.44 MB storage
COMPUTR: LORAN MS-DOS v.5
SOFTWARE: Word Perfect 5.1
COMPUTE: LOS PER-1993
PRICATION NUMBER: US/08/026,138E
FILING DATE: 26-FEB-1993
PRICATION NUMBER: JP 13355/1992
FILING DATE: 26-FEB-1993
APPLICATION NUMBER: JP 130878/1992
FILING DATE: 12-NUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Hamburg, C.Bruce
RESTRENCE/COCKET NUMBER: 22,389
REGISTRATION NUMBER: 12-NUG-1992
ATTORNEY/AGENT INFORMATION:
TELEFOWNUMICATION INFORMATION:
TELEFOWNUMICATION NUMBER: 22,389
REGISTRATION NUMBER: 22,389
REGISTRATION NUMBER: 12-NUG-1992
ATTORNEY HAD SECONDAL NUMBER: 12-NUG-1992
ATTORNEY AGENT NUMBER: 12-NUG-1992
ATTORNEY HAD SECONDAL NUMBER: 12-NUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE TYPE: brain
PUBLICATION INFORMATION:
AUTHORS: Masayoshi MISHINA
TITLE: NOVEL PROTEINS AND GENES CODING THE SAME
RELEVANT RESIDUES IN SEQ ID NO: 3: FROM 1 to 1239
FENCE 1239 AA; 135308 MW; 8004364 CN;
                                                                                                               1239 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 84; DB 1;
Pred. No. 1.58e+01
                                                                                                             PRT;
                                                                                                                                                                                                                                                 Sequence 3, Application US/08026138E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single strand
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (212) 986-2340
TELEFAX: (212) 953-7733
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1239 amino acids
                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 38.5%;
Matches 15; Conservative
4 AAVTILILILIPP-ALLSI 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: mouse
                                                                                                             US-08-026-138E-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                             XXXXXX
                                                                                      RESULT
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Sequence 6, Application PC/TUS9405365
GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Stephen L. Malaska, Immunex Corporation
51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER FEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Elem PC COMPATIBLE
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05365
FILING DATE: May 24, 1994
CLASSIFICATION:
APPLICATION NUMBER: -to be assigned-
FILING DATE: May 11, 1994
CLASSIFICATION NUMBER: 08/209,502
APPLICATION NUMBER: 08/209, 502
FILING DATE: March 7, 1994
CLASSIFICATION NUMBER: 08/209,502
FILING DATE: December 3, 1993
FILING DATE: December 3, 1993
                              235 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: NOWLER, 1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: AUGUST 12, 1993
CLASSIFICATION:
APPLICATION DATA:
APPLICATION WHERE: 08/068,394
FILING DATE: MAY 24, 1993
CLIASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
JENCE 235 AA; 26415 MW; 293990 CN;
                                                                                                                                                                                          Sequence 6, Application PC/TUS9405365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/111,758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION UNBRER: 32,655
REFRENCE/COCKET NUMBER: 2813
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 233-0644
                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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AC XXXXX

AC XXXXX

AX XXXXX

DE SEQUENCE 6, APPLICA

CC GENERAL INFORMAT:

CC APPLICANT:

CC APPLICANT:

CC APPLICANT:

CC COMPUTER READAN

CC COMPUTER READAN

CC COMPUTER:

CC COMPUTER
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Gaps

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8; Mismatches 15; Indels

4;

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APPLICANT: Thomason, Arlen R.;Nicholson, Margery
IIILE OF INVENTION: METHODS FOR PURIFICATION OF PLATELET-
DERIVED GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 5175255
APPLICANT: Thomason, Arlen R.;Nicholson, Margery
IIILE OF INVENTION: METHODS FOR PURIFICATION OF PLATELET-
DERIVED GROWTH FACTOR
                                                                                                                                                                      Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biologically Active
Polypeptide Fusion Dimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       282 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 81; DB 3; L
Pred. No. 2.56e+01;
9; Mismatches 4
                                                                                                                                                                    Score 81; DB 3; L
Pred. No. 2.56e+01;
9; Mismatches 4
                                                                                                                                                                                                                                                                                                                          261 AA
                                                                                                                                                                                                                                44 LQRLLQGDSGKEDGAELDLNMTRSHSGGELES 75
                                                                                                                                                                                                                                                  ||||||||: |: |: || | |:|||||
72 LQRLLQAN-GNH-AAGI-LTMGR-RAGAELEP 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 LQRLLQGDSGKEDGAELDLNMTRSHSGGELES 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08445847A
Patent No. 5705484
GENERAL INFORMATION:
APPLICANT: Thomason, Arlen R.
TITLE OF INVENTION: Biologically AC
TITLE OF INVENTION: Polypeptide Fus
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/25,344
FILING DATE: 23-MAR-1987
                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/25,344
FILING DATE: 23-MAR-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 241
SEQUENCE 261 AA; 29370 MW; 369384 CN;
                                                                                                                         LENGTH: 241
SEQUENCE 261 AA; 29326 MW; 367179 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08445847A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1840 Dehavilland Dr. CITY: Thousand Oaks STATE: California
                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 46.9%;
Matches 15; Conservative
                                                                                                                                                                    Query Match
Best Local Similarity 46.9%;
Matches 15; Conservative
                                               NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 91320-1789
                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 5175255.
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                                                                                                           SEQ ID NO:8
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5175255-2
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                                                                                                                                                                                                                     Gaps
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Patent No. 5175255
APPLICANT: Thomason, Arlen R.;Nicholson, Margery
IITLE OF INVENTION: METHODS FOR PURIFICATION OF PLATELET-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MURRAY, MARK J.:KELLY, JAMES D.
TITLE OF INVENTION: BIOLOGICALLY ACTIVE MOSAIC PROTEINS
NUMBER OF SEQUENCES: 34
CURRENT APPLICATION DATA:
                                                                                                                                                                       Score 82; DB 3; Length 220;
Pred. No. 2.18e+01;
....matches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 226;
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                                                                                                                                                                                                                                                                 ||||||:: |: | | : | | ::|:|||: ||
72 IQKLLQAN-GNHA-AGI-LTMGR-RAGAELEPHPCSGR 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 81; DB 3; L
Pred. No. 2.56e+01;
                                                                                                                                                                                                                                              23 LORLLHGDPGEEAGAELDLNMTRSHSGGELESLA-RGR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Mismatches
                                                                                                                                                                                                                                                                                                                                         245 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          261 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/319,776
FILING DATE: 07-0CT-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29 LORLLQGDSGKEDGAELDLNMTRSHSGGELES 60
                                                          NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/25,344
FILING DATE: 23-MAR-1987
                                                                                                                                                       238 AA; 26810 MW; 307752 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 226
ICE 245 AA; 27563 MW; 324570 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 926,149
FILING DATE: 05-AUG-1992
APPLICATION NUMBER: 379,239
FILING DATE: 11-7UL-1989
APPLICATION NUMBER: 941,970
FILING DATE: 15-DEC-1986
APPLICATION NUMBER: 896,485
FILING DATE: 3-AUG-1986
APPLICATION NUMBER: 705,175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           660,496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 12-OCT-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 9.0%;
Best Local Similarity 46.9%;
Matches 15; Conservative
                                                                                                                                                                                  Query Match 9.1%;
Best Local Similarity 44.7%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 25-FEB-
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                               DERIVED GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 5498600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 5175255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 5175255
                                                                                                                                        LENGIH: 220
                                                                                                                        SEQ ID NO:4:
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5498600-2
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5175255-8
                                                                                                                                                      SEQUENCE
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AC XX
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CC PR

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4

Gaps

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Sequence 2, Application PC/TUS9505512
GENERAL INFORMATION:
APPLICANT: Tonks, Nicholas K. and stman, Arne
TITLE OF INVENTION: Density Enhanced Protein Tyrosine
TITLE OF INVENTION: Phosphatase
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 233 South Wacker Drive, Suite 6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: United States of America

ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05512
                                                                                                                            1337 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27866/31954
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 1337 AA; 146192 MW; 9857375 CN;
                                                                                                                              PRT;
                                                                                                                                                                                                                                                        Sequence 2, Application PC/TUS9505512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1337 amino acids IYPE: amino acid
                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                     23 LLLLLLLPSPLMA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                      JT 15
PCT-US95-05512-2
                                                                                                                                                                        XXXXXX
                                                                                                        RESULT
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Query Match 8.9%; Score 80; DB 2; Length 1337; Best Local Similarity 46.4%; Pred. No. 3.01e+01; Matches 13; Conservative 4; Mismatches 10; Indels

1; Gaps

19 WA-LPLLLLLRGQILCAGGTPSPIPD 45

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Search completed: Thu Jul 30 09:28:43 1998 Job time: 7 secs.

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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu Jul 30 09:25:01 1998; MasPar time 2.04 Seconds 77.476 Million cell updates/sec Mar output not generated.

>US-08-938-548A-9 (1-27) from USO8938548A.pep 192 1 PGPPGLQGRLQANGNHAAGILIM 27 Description: Perfect Score: Sequence: Title:

PAM 150 Gap 15 Scoring table:

63816 segs, 5850866 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Mean 20.122; Variance 80.971; scale 0.249 a-issued 1:5_COMB 2:PCT9_COMB 3:backfiles Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Pred. No.	1.86e+01	2.26e+01	2.26e+01	5.81e+01	δ.	5.81e+01	5.81e+01	5.81e+01	5.81e+01	5.81e+01	8.42e+01	8.42e+01	8.42e + 01	8.42e+01	8.42e+01	8.42e+01	8.42e+01						
	_	Applicatio	Applicatio		Applicatio	, Applicati	, Applicati	, Applicati	14, Applicati	Æ.	, Applicati			5215895.	5215895.	Applicatio	Applicatio							
	Description	Sequence 3,	Sequence 4,	Sequence 10,	Sequence 2,	Sequence 2,	Sequence 4,	Sequence 2,	Sequence 8,	Sequence 4,	Sequence 4,	Sequence 4,	Sequence 14	Sequence 14	Sequence 14	٠,	4		Sequence 43,	ĭ	ċ	Patent No.	Sequence 2,	Sequence 2,
-	A	PCT-US91-0	PCT-US95-1	US-08-469-	PCT-US93-0	US-07-941-	US-07-949-	US-08-115-	US-08-792-	US-08-017-	US-08-115-	PCT-US93-0	US-08-165-	US-07-921-	US-07-745-	PCT-US94-1	US-07-941-	-924-10-SD	US-08-062-	US-07-924-	5215895-4	5215895-3	US-08-017-	US-07-949-
	DB	7	7	Н	~	Н	Н	Н	Ä	H	Н	~	-	н	Н	7	Н	Н	н	Н	m	m	-	Н
	Length	10	716	2509	199	199	199	199	199	199	296	296	296	296	296	296	296	26	27	27	199	199	199	199
dР	Query	34.4	33.9	33.9	31.3	31.3	31.3	31.3	31.3	31.3	31.3	31.3	31.3	31.3	31.3	31.3	31.3	30.2	30.2	30.2	30.2	30.2	30.2	30.2
	Score	99	65	65	9	9	9	9	9	9	9	9	9	9	9	9	9	28	28	28	28	58	28	28
	Result	,	7	٣	4	5	9	7	80	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

8.42e+01 8.42e+01 8.42e+01 8.42e+01 1.01e+02 1.01e+		
Patent No. 5498600. Patent No. 5175255. Patent No. 5175255. Sequence 1, Applicatio Sequence 2, Applicatio Sequence 3, Applicatio Sequence 1, Applicatio Sequence 2, Applicatio Sequence 1, Applicatio Sequence 2, Applicatio Sequence 2, Applicatio Sequence 1, Applicatio Sequence 2, Applicatio Sequence 2, Applicatio Sequence 2, Applicatio Sequence 2, Application Sequence 3, Application S	10 AA.	.04588 COMPLEXED LYMPHOTOXIN COMPLEXED LYMPHOTOXIN Fe 29th Floor 15-DOS 14.00 Version #1.25 191/04588 14.862 14.862
5498600-2 5175255-8 5175255-8 US-08-445- US-08-186- US-08-186- US-08-420- US-08-420- US-08-445- US-08-445- US-08-445- US-08-445- US-08-487- US-08-487- US-08-487- US-08-08- US-07-908- US-07-908- US-07-788- US-07-788- US-07-788- US-07-788- US-07-788- US-07-788- US-07-788- US-07-788- US-07-788- US-07-788- US-07-788- US-08-US-US-US-US-US-US-US-US-US-US-US-US-US-	ALIGNMENTS STANDARD; PRT;	
2 2 2 2 8 3 2 2 2 2 4 1 3 3 2 2 2 2 2 4 1 3 3 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	e e	quence 3, Application PC/TUS91 gquence 3, Application PC/TUS9 ENERAL INDEMATION: APPLICANT: Browning, Jeffre APPLICANT: Browning, Jeffre APPLICANT: Browning, Jeffre APPLICANT: Browning, Jeffre APPLICANT: Ware, Carl F. TITLE OF INVENTION: SURFACE NUMBER OF SEQUENCES: 3 CORRESPONDENCE ADDRESS: ADDRESSEE: C/O Fish & Near CITY: New York COUNTRY: USA ZIP: New YORK COUNTRY: USA ZIP: 10022-6250 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: BR PC Compation OPERATING SYSTEM: PC-DOS/ SOFTWARE: Patentin Releas CURRENT APPLICATION DATA: APPLICATION NUMBER: US OT/US FILLING DATE: 19910627 CLASSIPPICATION DATA: APPLICATION NUMBER: US OT/ FILLING DATE: 19910627 CLASSIPPICATION DATA: APPLICATION NUMBER: US OT/US FILLING DATE: 19910627 TELERHOWS: 122-115-0600 TELERHOWS: 122-115-0600 TELERHOR APPLICATION INFORMATION TELEFAX: 12-115-0674 TELEF
58888888888888888888888888888888888888	T PCT-US91-04588 XXXXXX	Sequence 3, Application PC/TUS91 Sequence 3, Application PC/TUS9 GENERAL INFORMATION: APPLICANT: Browning, Jeffre APPLICANT: Ware, Carl F. TITLE OF INVENTION: SURFACE NUMBER OF SEQUENCES: 3 CORRESPONDENCE ADDRESS: ADDRESSEE: C,O F1sh & New COTTY: New YORK COUNTY: New YORK COUNTY: USA ILP: 10022-6250 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: New YORK COMPUTER: DATE: PLOPSY STATE: New YORK COMPUTER: DATE: DATE: DATE: DATE: TELENG DATE: DATE: DATE: TELEBHORE HALEY JI. James F. REFERENCE/DOCKET NUMBER: DATE TELEBHORE CHARACTERISTICS: LENGTH: 10 amino acids TYPE: AMINO ACID TOPLOGY: UNKNOWN
	SUL	*#*#*888888888888888888888888888888888

P.O. Box 457

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COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/941,372

FLING DATE: 19920902

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Bak, MATY E:

REGISTRATION NUMBER: 31,215

REGISTRATION NUMBER: 1NDUS1

TELECOMMUNICATION INFORMATION:

MATTORNEY/AGENT NUMBER: 1NDUS1

TELECOMMUNICATION INFORMATION:

MATTORNEY/AGENT NUMBER: 1NDUS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 60; DB 1; Length 199;
Pred. No. 5.81e+01;
3; Mismatches 0; Indels
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Patent No. 5700664
GENERAL INFORMATION:
APPLICANT: Yang, Yu-Chung
APPLICANT: Bennett, Frances
TITLE OF INVENTION: A MAMMALIAN CYTOKINE, IL-11
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LEGAL AFFAIRS
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 199 AA
                                                    Spring House Corporate Center,
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APPLICATION NUMBER: US/07/949,516A
FILING DATE: 19-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 199 AA; 21429 MW; 188641 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/07949516A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (215) 540-9206
TELEFAX: (215) 540-818
INFORMATION FOR SEO ID 0: 2:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 199 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 31.3%;
Best Local Similarity 70.0%;
Matches 7; Conservative
CORRESPONDENCE ADDRESS
                                                                                                     Pennsylvania
: USA
                                                                            Spring House
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US-07-949-516A-4
                                                 STREET: S
CITY: Spr
STATE: Pe
COUNTRY:
                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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Patent No. 5460810
GENERAL INFORMATION:
APPLICANT: Williams, David A.
APPLICANT: Clark, Steven C.
TITLE OF INVENTION: Method of Treating Cell Damage or ITTLE OF INVENTION: Depletion
NUMBER OF SEQUENCES: 4
                                                                                                                   Sequence 2, Application PC/TUS9308247
GENERAL INFORMATION:
APPLICANT: Genetics Institute, Inc., ,
APPLICANT: CambridgePark Drive, ,
APPLICANT: Cambridge, MA 02140, USA
TITLE OF INVENTION: Method of Treating Cell Damage or
TITLE OF INVENTION: Depletion
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: 4 CORRESPONDENCE ADDRESSE: ADDRESSEE: ADDR
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5.81e+01; Indels
                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, P.O. Box 457
CITY: Spring House
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US93/08247 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               199 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,372
FILING DATE: 02-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: BAK, MARY E.
RESISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: INDIApct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 199 AA; 21429 MW; 188641 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31.3%; Score 60; 70.0%; Pred. No.
                                                                            Sequence 2, Application PC/TUS9308247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-9206
TELEPHONE: (215) 540-5818
INFORMATION FOR SED ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 199 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/07941372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 70.0% les 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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Local Similarity
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6 LOGRLORLLO 15
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Matches
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              Sequence 4, Application US/08017522A
Patent No. 5371193
GENERAL INFORMATION:
APPLICANT: BENNEY: FRANCES K
APPLICANT: YANG, YU-CHUNG
TITLE OF INVENTION: A MAMMALIAN CYTOKINE, IL-11
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: LEGAL AFFAIRS - GENETICS INSTITUTE, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08115680
Patent No. 5437863
GENERAL INFORMATION:
APPLICANT: Williams, David A.
TITLE OF INVENTION: Method of Treating Cell Damage or TITLE OF SEQUENCES:
AUGUSTESPONDENCES:
ADDRESSEE: Howson and Howson
                                                                                                                                                                                                                                                                                                                                                                                                                              e 60; DB 1; Length 199;
. No. 5.81e+01;
Mismatches 0; Indels
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Spring House Corporate Cntr, P.O. Box 457
                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/017,522A FILING DATE: 19930212
                                                                                                                                                                                                                                         FILING DATE: 19930212
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: MEINERT, M C
REGISTRATION NUMBER: 31,544
REFERENCE/DOCKET NUMBER: GI 5174A-DIV
TELEPHONE: (617) 876-1210 X8574
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  296 AA
                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
SEQUENCE 199 AA; 21429 MW; 188641 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 60;
Pred. No. 5
3; Mismat
                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
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Sequence 4, Application US/08017522A
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                                                                                                                                                                                                                                                                                                                                                         : 199 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of COMPUTER: IBM PC comp
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Best Local Similarity 70.0%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                CAMBRIDGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129 LQARLDRLLR 138
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                                                                                                                                                    COUNTRY:
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GENERAL INFORMATION:
APPLICANT: Genetics Institute, Inc., ,
APPLICANT: 87 CambridgePark Drive, ,
APPLICANT: CambridgePark Drive, ,
APPLICANT: Cambridge, MA 02140, USA
TITLE OF INVENTION: Method of Treating Cell Damage or
TITLE OF INVENTION: Depletion
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE: ADDRESSE: ADDRESSEE: Spring House Corporate Cntr, P.O. Box 457
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                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATES: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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SOFTWARE: PatentIn Release #1.0, Version #1.25
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Pred. No. 5.81e+01;
3; Mismatches 0
                                                                                                                                                                                                           CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,372
FILING DATE: 02-SEP-1992
ATORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
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APPLICATION NUMBER: PCI/US93/08247
                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: INDIAusa
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-506
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,372
                                                                                                                    SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/115,680 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 296 AA; 31769 MW; 414378 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 296 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
ZIP: 19477
COMPUTER READABLE FORM:
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70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
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CLASSIFICATION:
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TOPOLOGY: linear
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                                                                                               Sequence 14, Application US/07745382
Patent No. 5270181
GENERAL INFORMATION:
APPLICANT: McCoy, John
APPLICANT: LaValie, Edward
TITLE OF INVENTION: Peptide and Protein Fusions To
TITLE OF INVENTION: Phioredoxin and Thioredoxin-Like Molecules
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/745,382
FILING DATE: 19910814
CLASSIFICATION DATA:
RELING APPLICATION DATA:
APPLICATION NUMBER: US 07/652,531
FILING DATE: 06-FEB-1991
ATTORNEY/AGENT INFORMATION:
WANTE: COMPANDEMENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               296 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 60; DB 1; Lengard. No. 5.81e+01; 3; Mismatches 0;
                           296 AA.
                                                                                                                                                                                                                                                                                                                                                                           NAME: CSETY, LUANN
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: G15188A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14, Application PC/TUS9414179 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
JENCE 296 AA; 31769 MW; 414378 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application PC/TUS9414179
                                                                                  Sequence 14, Application US/07745382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGIH: 296 amino acids TYPE: AMINO ACID
                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.3%;
ilarity 70.0%;
Conservative
                                                                                                                                                                                                                       STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                            COUNTRY: U.S.A.
ZIP: 02140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     226 LQARLDRLLR 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 LOGRIQRILQ 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JT 15
PCT-US94-14179-14
                  JT 14
US-07-745-382-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                              XXXXXX
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                 RESULT
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CC APPLICANT: Dislate. Smith, Elizabeth
CC APPLICANT: Crait, Kathleen
CC APPLICANT: Crait, Kathleen
CC APPLICANT: Crait, Kathleen
CC TILLE OF INVENTION: THIOREDOXIN. INTOREDOXIN. INTOREDOXIN. THOREDOXIN. THIOREDOXIN. THIOREDOX
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Thu Jul

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MasPar time 3.90 Seconds 106.277 Million cell updates/sec Thu Jul 30 09:22:53 1998;

lar output not generated.

WPsrch_pp

>US-08-938-548A-9 (1-27) from US08938548A.pep 192 Description: Perfect Score: Title:

1 PGPPGLQGRLQRLLQANGNHAAGILTM 27 Sequence:

PAM 150 Gap 15 Scoring table:

124785 segs, 15338987 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-geneseg31-2
l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27

Mean 21.806; Variance 86.670; scale 0.252 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

)		d			SUMMARIES		
Result		Ouery					
No.	Score	Match	Match Length DB	BO	£	Description	Pred. No.
-	99	34.4	10	4	R20235	"p33" N-terminal (2).	5.96e+01
7	65	33.9	716	18	R99737	Retinoid X receptor i	7.19e+01
٣	65	33.9	2509	24	W32881	Protein (OA-519) cros	7.19e+01
4	64	33.3	549	16	R92050	KM31-7 precursor.	8.67e+01
Ŋ	64	33.3	1477	13	R67691	S. cerevisiae scaur2R	8.67e+01
9	64	33.3	1477	22	W10424	Saccharomyces cerevis	8.67e+01
7	63	32.8	878	m	R13793	Ecdysone receptor.	1.04e+02
8	63	32.8	878	9	R32889	DHR23alpha protein.	1.04e+02
6	61	31.8	32	Н	R00579	New polypeptide based	1.51e+02
10	61	31.8	248	Н	R06331	Human alveolar surfac	1.51e+02
11	61	31.8	248	-	P80694	Sequence deduced from	1.51e+02
12	61	31.8	248	~	P70662	35kd pulmonary surfac	1.51e+02
13	9	31.8	248	~	P70663	35kd pulmonary surfac	1.51e+02
14	61	31.8	248	m	P60665	Sequence of human alv	1.51e+02
15	61	31.8	248	ო	P60666	Genomic sequence of h	1.51e+02
16	61	31.8	248	m	P60441	Plasmid pASPc-SV(10)	1.51e+02
17	61	31.8	248	m	P60442	Plasmid pASPcq-SV(10)	1.51e+02
18	61	31.8	248	Н	P82980	Sequence deduced from	1.51e+02
19	61	31.8	248	7	R05091	Vector PSP 35K-1A-10	1.51e+02

~	~	~	2	~	2	~	2	2	2	~	2	2	2	2	~	~	~	21	2	2	2	2	~	2	2
51e+0	51e+0	1e+0	1e+0	1e+0	81e+02	1e+(1e+(81e+05	1e+(1e+0	1e+(1e+(1e+0	1e+0	1e+0	1e+(1e+(81e+02	1e+(81e+0	18e+0	18e+0	18e+0	18e+0	18e+02
1.5	1.5	1.5	1.5	1.5	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	2.1	2.1	2.1	2.1	2.1
Human 32K ASP encoded	Human 32K ASP encoded	Human 32K alveolar su	Genomic sequence of h	Human 32K ASP encoded	Human adipogenesis in	Human adipogenesis in	Human interleukin-11	Human interleukin-11	Sequence of a cytokin	Human Interleukin-11	Human adipogenesis in	Human interleukin-11.	E.coli thioredoxin-hu	Thioredoxin from PALT	Thioredoxin/des-Pro-I	Thioredoxin-Interleuk	Fusion protein of IL-		M. tuberculosis RNA p	Virulence-associated	Thermus aquaticus hea	LexA/NuMA fusion prot	A fusi	synthas	Platenolide synthase
R04215	R04216	R04212	P60661	R04217	R43261	R43262	W02202	R75337	R24436	R50176	R43260	R12314	R45916	R26051	R75762	R50177	R26213	R76812	W05831	R76480	R49835	W21732	W21731	W22608	W23718
Н		 1	m	~	æ			14															23	25	25
248	248	271	271	271	169	177	178	178	199	199	199	199	296	296	296	296	296	296	528	530	510	2192	2272	3724	2
∞.	ω.	ω.	∞.	ω.	۳.	۳.	m.	1.3	۳.	1.3	1.3	۳.	1.3	31.3	31.3	m.	1.3	1.3	۳.	۳.	۲.	۲.	۲.	٠.	.7
31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	30	30	30.7	30	30
61	61	61	61	61	9	9	9	9	9	9	9	9	9	9	9	9	9	09	9	9	29	29	59	59	23
50	21	22	23	24	25	56	27	78	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
					_																				

ALIGNMENTS

The Total 1991; U04588.

R 27-JUN-1990; U05-544862.

R 27-JUN-1990; U05-544862.

R EDGC) BIOGEN INC.

REGC) UNIV OF CALIFORNIA.

REGC) UNIV OF CALIFORNIA.

IN Proming J, Ware CF;

WPI; 92-041521/05.

In Paphotoxin, useful as antiinflammatory agent, tumour growth inhibitor. T-cell inhibitor or activator.

T inhibitor. T-cell inhibitor or activator.

C laim 1; Page 60; 75pp; English.

A protein, designated p33, is found on the surface of several types of lymphocyte ecils, including OKT3-stimulated primary T-cells, antigen-specific IL-2 dependent CT1 clones, and a PMA-stimulated human T-cell hybridoma, II-23.D7. It forms a novel complex with complex vict in RNPOACOM (IT). The N-terminal of the p33 protein contains the sequence represented in RN2024 or RN20335. The sequence at the 6th cycle appeared to be a mixt. of both G and I indicating possible between the p33 protein may have one of these sequences or Score 66; DB 4; Length 10; Pred. No. 5.96e+01; 1; Mismatches 0; Indels /note= "polymorphism - see CC" 24-APR-1992 (first entry) "p33" N-terminal (2). MAP; lymphocyte; IL-2; CTL; polymorphism. Location/Qualifiers Z T 1 R20235 standard; Protein; 10 R20235; Key misc_difference 6 Sequence 10 AA; Homo sapiens WO9200329-A. **39-JAN-1992** RESULT

34.4%; Similarity 88.9%; 8; Conservative Query Match Best Local Similarity ||:|||||| 5 GLQGRLQRL 13 1 glegrigrl 9 ద ò

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Gaps

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0; Indels

RESULT

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domain
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    NAME OF THE PROPERTY OF THE PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is the protlen product of the Saccharomyces cerevisiae AL33-18C (FERM BP-5529) aureobasidin resistance gene scaurz, the claimed promoter of which can be used for the effective expression of genes encoding proteins, antisense DNA or RNA, decoy genes or ribozymes in yeast, e.g. for the industrial scale production of proteins for drug or food use. The promoter's transcription can be regulated by proteins encoded by the plaiotropic drug resistance gene, PDR, and it can be used for culture in a complete nutritive medium.
                                                                   Disclosure; Page 77-84; 110pp; English.
Saccharomyces cerevisiae DKD5D, which is sensitive to aureobasidin, was mutagenized with EMS and genomic libraries of 2 resistant strains were prepared. Resistant gene scauriR (Q75956) from the Other. A DNA fragment of scauri was used as a probe to isolate a sensitive gene, scauris (Q75956), from the other. T852A mutation leading to a F158Y conversion gave rise to the resistance of scaurir.
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae aureobasidin resistance protien scaur2.
Aureobasidin; resistance; scaur2; promoter; expression; protein;
DNA; RNA; antisense; decoy; qene; ribozyme; yeast; industrial; PDR;
pleiotropic; production; transcription; regulation; drug; food.
Saccharomyces cerevisiae AL33-18C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aureobasidin resistance gene, scaur2, promoter - useful for effective prodn. of genes encoding proteins, antisense DNA or RNA, decoy genes or ribozymes in yeast Example 3; Pages 31-38; 48pp; Japanese.
New genes regulating aureobasidin sensitivity - used to develop prods. for the diagnosis and treatment of diseases such as
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                                                                                                                                                                                                                                                                                                                                           Length 1477;
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Pred. No. 8.67e+01;
                                                                                                                                                                                                                                                                                                                                        Score 64; DB 13; Length 147
Pred. No. 8.67e+01;
5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ecdysone receptor.
Insect steroid receptor; EcR; hormone; DHR23.
Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
264..329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W10424 standard; Protein; 1477 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R13793 standard; Protein; 878 AA. R13793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-DEC-1996.
27-MAY-1995; J01415.
30-MAY-1995; JP-154094.
(TAKI ) TAKARA SHUZO CO LID.
Kato I, Okado T, Takesako K;
WPI; 97-034382/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        518
                                                                                                                                                                                                                                                                                                                                                                                                                                       499 grlqslleapeddpngmiem 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 GRLORLLOANGNHAAGILTM 27
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                                                                                                                                                                                                                                                                                                                                        Query Match 33.3%;
Best Local Similarity 40.0%;
Matches 8; Conservative
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Best Local Similarity 40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-AUG-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        499 grlqslleapeddpnqmiem
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                                                    mycoses
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  셤
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for induced expression of heterologous genes
Disclosure; Fig 1; 45pp; English encounter, English encounter, English encounter, English encounter, English encounter, Fig 1; 45pp; English encounter, Engli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding insect steroid receptors - and ligands, for use as benign inducing factors
Claim 24; Page 103; 126pp; English.

The amino acid sequence codes for the (20-0H) ecdysone receptor protein which is part of the insect steroid receptor superfamily. It can be used to screen for ligands specific for the insect steroid receptors which can be used as highly specific and highly active pesticides which are biodegradable. See also Ri3791-Ri3794.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ecdysteroid, receptor; DHR23alpha; Drosophila; steroid; receptor;
ligand-dependant; transcription factor; mammalian cell; hormone;
ecdysone response element; ecdysone.
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Pred. No. 1.04e+02;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 63; DB 6; Length 878;
Pred. No. 1.04e+02;
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/note= "zinc-finger DNA-binding domain
431..651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Putative DNA-binding domain"
                                                                                                               /note= "hormone-binding domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
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281..330
                                                                                                                                                                                                                                                                                                                                          Hogness DS, Koelle MR, Segraves WA, WPI; 91-281480/38.
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R32889 standard; Protein; 878 AA.
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Similarity 64.3%;
9; Conservative
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Best Local Similarity 64.3%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                      26-FEB-1990; US-485749.
(STRD ) LELAND STANFORD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster
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08-AUG-1991; US-742127.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 PPGLOGRIORLIOA 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPGLQGRLQRLLQA 16
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Best Local Similarity
                                                                                                                                                                                                                                            15-FEB-1991; U01189
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Pulmonary surfactant proteins - used for treating Hyaline Membrane Disease or Respiratory Distress Syndrome.
Claim 1; Page 33-34; 50pp; English.
Gene product may be used in treatment of Hyaline Membrane Disease and Respiratory Distress Syndrome (RDS) in both premature infants and adults eg. cardio-pulmonary operations. The protein products may also be used to raise diagnostic antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pulmonary surfactant proteins - used for treating Hyaline Membrane Disease or Respiratory Distress Syndrome. Claim 1; Page 34A-B; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene product may be used in treatment of Hyaline Membrane Disease and Respiratory Distress Syndrome (RDS) in both premature infants and adults eg. cardio-pulmonary operations. The protein products may also be used to raise diagnostic antibodies.

Sequence 248 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-APR-1991 (first entry)
35kd pulmonary surfactant protein.
Hyaline membrane disease; respiratiory distress syndrome; RDS.
                                   35kd pulmonary surfactant protein.
Hyaline membrane disease; respiratiory distress syndrome; RDS.
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Pred. No. 1.51e+02;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                              (GENE-) Genetics Institute Inc. (BRIG-) Brigham and Women's Hospital. Taeusch HW, Cobs KA, Steinbrink DR, Floros J, Phelps DS; WPI: 87-108682/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GENE.) Genetics Institute Inc.
(BRIG-) Brigham and Women's Hospital.
Tacusch HW, Cobs KA, Steinbrink DR, Floros J, Phelps DS;
WPI: 87-108682/15.
N-PSDB; N1010.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JT 14 P60665 standard; Protein; 248 AA. P60665; P100665; P60665; P60665; P60665 Sequence of human alveolar surfactant protein (hASP)
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 61; DB 2; Lv
Pred. No. 1.51e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
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Best Local Similarity 60.0%;
                  (first entry)
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                                                                                                               us-ark-1987.
26-SEP-1986; UO2034.
26-SEP-1985; US-781130.
15-AUG-1986; US-897183.
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26-SEP-1986; U02034.
26-SEP-1985; US-781130.
15-AUG-1986; US-897183.
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Best Local Similarity
Matches 9; Conserv
                                                                      Homo sapiens.
WO8702037-A.
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WO8702037-A.
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Genomic sequence of human alveolar surfactant protein (hASP)
encoded by genomic DNA, used to obtain pASPcg-SV(10)
Regulatable expression system.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example; Fig 5; 94pp; English.
A regulatable expression system for a coding sequence is The system can process genomic as well as intronless DNA. Sequence 248 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example; Fig 6; 94pp; English.

A regulatable expression system for a coding sequence is The system can process genomic as well as intronless DNA. Sequence 248 AA;
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Pred. No. 1.51e+02;
3; Mismatches 3; Indels
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Pred. No. 1.51e+02;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                          (BIOT-) BIOTECHN RES PARTNE.
(KUSH/) KUSHNER P J.
Kushner PJ. Cofer CL, Friedman J, Talmadge KD;
WPI: 86-228888/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-FEB-1985; US-701296.
13-FEB-1985; US-7011296.
(BIOT-) BIOTECHN RES PARTNE.
(KUSH/) KUSHNER P J.
KUSHNEY PJ. Cofer CL. Friedman J, Talmadge KD;
N-PSDB; N60572.
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                                                                            Location/Qualifiers
1..20
21..248
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P60666 standard; Protein; 248 AA.
P60666;
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on pMT(E):HS and pASPc-SV(10) Regulatable expression system
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60.0%;
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31.8%;
Best Local Similarity 60.0%;
Matches 9; Conservative
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GPPGLQGRLQRLLQA 16
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25-NOV-1985; US-801674.
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Matches 9; Conserv
                                                        Homo sapiens.
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WO8604920-A.
28-AUG-1986.
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Gaps



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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu Jul 30 09:20:43 1998; MasPar time 3.05 Seconds 271.021 Million cell updates/sec

>US-08-938-548A-8 (1-33) from US08938548A.pep 256 lar output not generated.

1 OPLPDCCROKTCSCRLYELLHGAGNHAAGILTL 33 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

69111 seqs, 25083644 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

swiss-prot35 1:swiss1 Database:

Mean 31.693; Variance 44.992; scale 0.704 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	5.12e-02	1.20e-01	2.76e-01	4.17e-01	6.26e-01	6.26e-01	1.40e+00	1.40e+00	2.07e+00	2.07e+00	2.07e+00	2.07e+00	3.06e+00	3.06e+00	4.51e+00	4.51e+00	4.51e+00	4.51e+00	4.51e+00	4.51e+00	4.51e+00	6.60e+00	6.60e+00
Description	CASPASE-11 PRECURSOR (PUTATIVE TRANSMEMBRANE	PUTATIVE ACID PHOSPHAT	60S RIBOSOMAL PROTEIN	SPERM MITOCHONDRIAL CA	PUTATIVE FORKHEAD-RELA	IG ALPHA CHAIN C REGIO	MEIOTIC RECOMBINATION	UDP-GLUCOSE 4-EPIMERAS	UDP-GLUCOSE 4-EPIMERAS	PHOSPHORIBOSYLAMINOIMI	INTERFERON-ACTIVATABLE	HYPOTHETICAL PROTEIN M	MITOCHONDRIAL INHERITA	OMEGA-AGATOXIN IIIA.	OMEGA-AGATOXIN IVB PRE	BOLA PROTEIN HOMOLOG.	AGOUTI SWITCH PROTEIN	AGOUTI SWITCH PROTEIN	AGOUTI SWITCH PROTEIN	VACUOLAR PROCESSING EN	PROTEIN ECSC.	ANGIOTENSINOGEN PRECUR
ΩI	ICEB_MOUSE	NMA_HUMAN	PPAW_CAEEL	R10A_TRYBR	MCS_MOUSE	YULZ_CAEEL	ALC_RABIT	RE11_SCHPO	GALE_RAT	GALE_HUMAN	PURK_PSEAE	IFI5_MOUSE	Y115_METJA	MD12_SCHPO	TX03_AGEAP	TX4B_AGEAP	BOLA_HAEIN	AGSW_VULVU	AGSW_MOUSE	AGSW_HUMAN	VPE_VICSA	ECSC_BACSU	ANGT_MOUSE
DB	-	H	-	Н	m	Н	н	Н	ч	ч	-	П	H	-		Н	Н	ч	÷,			ч	Н
Length	373	260	450	214	197	461	299	923	347	348	360	425	155	273	16	83	103	125	131	132	493	236	477
Query Match	29.3	28.5	27.7	27.3	27.0	27.0	26.2	26.2	25.8	25.8	25.8	25.8	25.4	25.4	25.0	25.0	25.0	25.0	25.0	25.0	25.0	24.6	24.6
Score	75	73	7.1	70	69	69	67	29	99	99	99	99	65	65	64	64	64	64	64	64	. 64	63	63
Result	,	7	m	4	S	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23

29.3%; Score 75; DB 1; Length 373;

Query Match

6.60e+00	9.61e+00	9.61e+00	9.61e+00	9.61e+00	9.61e+00	1.39e+01	1.39e+01	1.39e+01	1.39e+01	1.39e+01	1.39e+01	1.39e+01	1.39e+01	2.01e+01	2.01e+01	2.01e+01	2.01e+01	2.01e+01	2.01e+01	2.01e+01	2.01e+01
TETRACYCLINE RESISTANC	UNC-6 PROTEIN PRECURSO	GLUTAMATE (NMDA) RECEP	GLUTAMATE (NMDA) RECEP	SPA2 PROTEIN.	MYOSIN HEAVY CHAIN, NO	GENE 34 PROTEIN.	UREASE OPERON URED PRO	UREASE OPERON URED PRO	HYPOTHETICAL PROTEIN K	TUBULIN BETA CHAIN.	PRPD PROTEIN.	GLYCINE BETAINE TRANSP	DNA REPAIR PROTEIN RAD	HYPOTHETICAL 37.9 KD P	MITOGEN-ACTIVATED PROT	HYPOTHETICAL 51.7 KD P	TETRACYCLINE RESISTANC	HYPOTHETICAL 118.6 KD	DNA POLYMERASE (EC 2.7	HYPOTHETICAL 133.0 KD	THYROGLOBULIN PRECURSO
TET9_ENTFA	UNC6_CAEEL	NME1_RAT	NME1_MOUSE	SPA2_YEAST	MY SO_HUMAN	VG34_HSVEB	URED_KLEAE	URED_KLEPN	Y129_HUMAN	TBB_TRYBR	PRPD_SALTY	BETP_CORGL	RAD5_YEAST	YHO5_YEAST	NTF6_TOBAC	YMT1_CAEEL	TETM_UREUR	YAF3 SCHPO	DPOL_ADE07	YIC6_YEAST	THYG_BOVIN
Н	-1	H	٦	-	٦	-	н	Н	~4	H	н	H	Н	-	H	н	-	Н	Н	-1	-
639	612	1464	1464	1466	1976	160	270	270	406	442	483	595	1169	334	371	471	639	1039	1122	1150	2769
24.6	24.2	24.2	24.2	24.2	24.2	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.8	23.4	23.4	23.4	23.4	23.4	23.4	23.4	23.4
63	62	62	62	62	62	61	61	61	61	61	61	61	61	9	9	9	9	9	9	9	9
24	25	56	27	28	29	30	31.	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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4; Mismatches
                                                                                                                                                                                                                                                                                                                                                   923 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE; 97231330.
LI Y.F., NUMATA M., WAHLS W.P., SMITH G.R.;
MOL. MICROBIOL. 23:869-878(1997).
EMBL; U70737; G1619901; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   347 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       232 CCDIMRCLCLIVNKLSEKSNQTAEILVL 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                         HSSP; P01857; 1PFC.
PROSITE; PS00290; IG_MHC; 2.
IMMUNOGLOBULIN C REGION.
                                                                                                                                                                                                                     26.2%;
                                                                                                                                                                                                                                              7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE-SKELETAL MUSCLE;
MEDLINE; 90384840.
                                                              IMMUNOLOGIC SYSTEM.
                                                                                                  CHAIN HAPLOTYPE.
EMBL; X00353; G1576; -.
PIR; A02174; AHRB.
                                                                                                                                                                                                                                                                       44 PFPDCCPANSCCTC 57
                                                                                                                                                                                                                                                                                               2 PLPDCCRQKTC-SC 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GALACTOSE 4-EPIMERASE)
                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                RE11_SCHPO
Q92380;
                                                                                                                                                                               NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LT 9
GALE_RAT
P18645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEIOSIS
                                                                                                                                                                                                                                  Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
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                                                                                                                                                                                                                     ä
                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; ACOELOMATES; NEWATODA; SECERNENTEA; RHABDITIDA.
     01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
IG ALPHA CHAIN C REGION (FRAGMENT).
ORYCTOLAGUS CUNICULUS (RABBIT).
EUKARYOTA: METAZOA: CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; LAGOMORPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                     5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 69; DB 1; Length 461; Pred. No. 6.26e-01;
                                                                                                                                                                                          DB 1; Length 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Indels
                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
PUTATIVE FORKHEAD-RELATED TRANSCRIPTION FACTOR F26A1.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBMITTED (JUN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; UZ7312; G860690; -.

WORMPEP; F26A1.2; CE02683.

PROSITE; PS00655; FORK_HEAD_1; 1.

PROSITE; PS500589; FORK_HEAD_2; 1.

PROSITE; PS50039; FORK_HEAD_3; 1.

HYPOTHETICAL PROTEIN; DNA-BINDING; NUCLEAR PROTEIN; TRANSCRIPTION REQUEATION.

BUNA_BIND 171 262 FORK-HEAD.

SEQUENCE 461 AA; 54171 MM; FB2C37B7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SULT 7
ALC_RABIT STANDANC,
DO1879;
T 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
T 21-JUL-1996 (REL. 11, LAST ANNOTATION UPDATE)
T T-TT-1991 (REL. 17, LAST ANNOTATION UPDATE)
T TRIPION (FRAGMENT).
                                                                                                                                                                                                       Pred. No. 6.26e-01;
                                                                                                                                                     SELENIUM.
4E56990C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCÁTION: NUCLEAR (PÓTENTIAL).
-!- SIMILARITY: CONTAINS A FORK-HEAD DOMAIN.
                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                          461 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
STRUCTURE OF THE SPERM MITOCHONDRIA
                                                                                                                                                                                           Score 69;
                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQI
01-NOV-1997 (REL. 35, LAST ANN
                                                                                                                                       17 17 5
34 34 8
197 AA; 21015 MW;
                                                                                                                                                                                           27.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 27.0%;
Best Local Similarity 35.3%;
Matches 6; Conservative
                                                                                                                                                                                                         Similarity 71.4%;
10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                221 RHVLCKCQLFDVLQVEG 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |: | |:|: | ROKTCSCRLYELLHGAG 24
                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                              123 PLKPPCCPQK-CSC 135
                                                                                                                                                                                                                                                                 2 PL-PDCCRQKTCSC 14
                                                                                                                                                                                                     Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE; 84144059.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                           T 6
YUL2_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FULTON L.;
                                                                                                                                                      BINDING
                                                                                                                                                                                           Query Match
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셤 ò 019802;

RESULT TO THE SULT TO THE SULT

Matches

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-!- THIS IMMUNOGLOBULIN BELONGS TO THE IGA-G SUBCLASS. IT WAS ISOLATED FROM A RABBIT HOMOZYGOUS FOR A2, N80, DE12,15, F71, G75 HEAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
KNIGHT K.L., MARTENS C.L., STOKLOSA C.M., SCHNEIDERMAN R.D.;
NUCLEIC ACIDS RES. 12:1657-1670(1984).
--- PUNCTION: IG ALPHA IS THE MAJOR IMMUNOGLOBULIN CLASS IN BODY
SECRETIONS. IT MAY SERVE BOTH TO DEFEND AGAINST LOCAL INFECTION
AND TO PREVENT ACCESS OF FOREIGN ANTIGENS TO THE GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZESCHNIGK M., WILCKEN-BERCMANN B., STARZINSKI-POWITZ A.;
NUCLEIC ACIDS RES. 18:5289-5289(1990).
-1- FUNCTION: CATALYZES TWO DISTINCT BUT ANALOGOUS REACTIONS: THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ij
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01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 26.2%; Score 67; DB 1; Length 923; Best Local Similarity 35.7%; Pred. No. 1.40e+00; Matches 10; Conservative 6; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 67; DB 1; LA Pred. No. 1.40e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     923 AA; 107418 MW; B51C7725 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   299 AA; 32256 MW; 594CED7C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
MEIOTIC RECOMBINATION PROTEIN REC11.
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                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 96337999.

MEDLINE; 96337999.

BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D., SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCAYNE J.D., KERLAVAGE A.R., DOUGHERY' B.A., TOMB J.-F., ADAMS M.D., REICH C.I., OVERBEEK R., KIRKNESS E.F., WEINSTOCK K.G., MERRICK J.M., GLODEK A., SCOTT J.L., GEOGRAGEN N.S.M., WEIDMAN J.F., FURRMANN J.L., NGUYEN D., UTTERBACK T.R., KELLEY J.M., PETERSON J.D., SADOW P. W., HANNA M.C., COTTON M.D., ROBERTS K.M., SMITH H.O., WOBSE C.R., VENTER J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                     METHANOCOCCUS JANNASCHII.
ARCHAEBACTERIA; EURYARCHAEOTA; METHANOCOCCALES; METHANOCOCCACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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Pred. No. 3.06e+00;
6; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BERGER K.H., SOGO L.F., YAFFE M.P.;
SUBMITTED (NOV-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- SIMILARITY: TO YEAST MDM12.
EMBL. U64674; G1655884; -.
SEQUENCE 273 AA; 30517 MW; 9024B3CC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 65; DB 1; Lv
Pred. No. 3.06e+00;
2; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          155 AA; 17727 MW; 9D9D61E8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MD12_SCHPO STANDARD; PRT; 273 AA. 092377; 01-NOV-1997 (REL. 35, CREATED) 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE) 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE) MITOCHONDRIAL INHERITANCE COMPONENT MDM12.
                                                                                                                                  LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (REL. 27, CREATED)
(REL. 27, LAST SEQUENCE UPDATE)
(REL. 28, LAST ANNOTATION UPDATE)
                                     155 AA
                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                         (REL. 35, CREATED)
(REL. 35, LAST SEQ:
(REL. 35, LAST ANN
                                                                                                                                                                                                       HYPOTHETICAL PROTEIN MJ0115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 25.4%;
Best Local Similarity 53.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 25.4%;
Best Local Similarity 53.3%;
Matches 8; Conservative
                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 CCKITKPCPYRDYEL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 CCR-QKTCSCRLYEL 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U67469; G1498882;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213 LLHGTGEHASSVI 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19 LLHGAGNHAAGIL 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OMEGA-AGATOXIN IIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                              Y115_METJA
Q57579;
01-NOV-1997 (
                                                                                                                                  01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-1993
01-FEB-1994
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01-0CT-1993
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RESOLT
11D Y1
11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT ID MD
AC 099
DT 011
DT 01
DD DT 01
DE MI
GN MD
OC EU
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VENEMA V.J., SWIDEREK K.M., LEE T.D., HATHAWAY G.M., ADAMS M.E.;
J. BIOL. CHEM. 267:2610-2615(1992).
-!- FUNCTION: OMEGA-AGATOXIN ARE ANTAGONIST OF VOLTAGE-SENSITIVE
CALCIUM CHANNELS. THEY BLOCK INSECT NEUROWUSCULAR TRANSMISSION
PRESYNAPTICALLY. POTENT BLOCKER OF N- AND L-TYPE CALCIUM CHANNELS.
                                                                                                                                                                                                                                                                                                                                    -!- PIM: SIX DISULFIDE BONDS ARE PRESENT (PROBABLE).
PIR: A42335; A42335; A4235; A2235; A8235; A82300XIN: CALCUM CHANNEL INHIBITOR; PRESYNAPTIC NEUROTOXIN.
SEQUENCE 76 AA; 8518 MW; C7EAOEL2 CR032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
AGELENOPSIS APERTA (FUNNEL-WEB SPIDER).
EUKARYOTA; METAZOA; ARTHROPODA; CHELICERATA; ARACHNIDA; ARANEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 64; DB 1; Length 76; Pred. No. 4.51e+00; 6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 QCCRRNGYCSCYSLFGYLKSG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 DCCROKT-CSC-RLYELLHGA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25.0%;
similarity 38.1%;
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 8; Conser
                                                                                                                       TISSUE-VENOM;
MEDLINE; 92129351.
                                                                                     SEQUENCE
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在各种社会的现在分词 医克格特氏 医克格特氏氏征 医克格特氏病	,	***************************************
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu Jul 30 09:21:12 1998; MasPar time 5.80 Seconds 239.700 Million cell updates/sec lar output not generated.

>US-08-938-548A-8 (1-33) from USO8938548A.pep 256 1 QPLPDCCRQKTCSCRLYELLHGAGNHAAGILTL 33 Description: Perfect Score: Sequence: Title:

PAM 150 Gap 11 Scoring table:

140542 seqs, 42109429 residues

Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptrembl5
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Mean 30.295; Variance 46.908; scale 0.646

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	5.22e-02	1.77e-01	2.65e-01	2.65e-01	2.65e-01	2.65e-01	3.94e-01	3.94e-01	8.65e-01	8.65e-01	1.87e+00	1.87e+00	1.87e+00	3.99e+00	5.80e+00	5.80e+00	8.38e+00	8.38e+00	8.38e+00	8.38e+00	
Description	PORCINE MEMBRANE COFAC	F14B4.1 (FRAGMENT).	T05A1.3.	PHOSPHOINOSITIDE 3-KIN	PHOSPHOINOSITIDE 3-KIN	PHOSPHOINOSITIDE 3-KIN	3' ORF.	DNA GYRASE B SUBUNIT.	SIMILAR TO GALACTOKINA	DYSTROPHIN (FRAGMENT).	TET.	TETRACYCLINE RESISTANC	TYROSINE KINASE.	HOMOLOGUE OF REGULATOR	KAP5.5 KERATIN PROTEIN	BETA-D-FRUCTOFURANOSID	COSMID C04E6.	FROM BASES 996879 TO 1	1-CARBOXY - 3-CHLORO-3, 4	SELD PROTEIN.	
Ð	002839	093473	022187	024453	001938	024209	061639	033367	001969	091493	048791	048712	090975	P94426	028584	013388	001473	P75863	044258	018373	
88	4	٣	ო	m	m	m	10	σ	ო	12	σ	σ	12	σ	4	Н	٣	σ	σ	m	
Ouery Match Length DB	363	750	683	1876	1876	1876	147	815	426	883	641	646	1382	479	197	589	310	369	397	398	
Query	30.1	28.9	28.5	28.5	28.5	28.5	28.1	28.1	27.3	27.3	26.6	26.6	26.6	25.8	25.4	25.4	25.0	25.0	25.0	25.0	
Score	77	74	73	73	73	73	72	72	70	70	89	68	89	99	65	65	64	64	64	64	
Result No.	1	7	m	4	Ŋ	φ	7	ω	σ	10	11	12	13	14	15	16	17	18	19	50	

8.38e+00	1.21e+01	1.21e+01	1.21e+01	1.21e+01	1.21e+01	1.21e+01	1.21e+01	1.21e+01	1.21e+01	1.21e+01	1.21e+01	1.21e+01	1.73e+01	1.73e+01	1.73e+01	1.73e+01	1.73e+01	1.73e+01	1.73e+01	1.73e+01	1.73e+01	1.73e+01	2.47e+01	2.47e+01	
_	REPRESSOR/INDUCER PROT 1	COSMID C27A2.	RIBONUCLEASE.	T21B10.6.	F21C3.1.	AMINO ACID TRANSPORTER :	TETRACYCLINE RESISTANC	TETRACYLINE RESISTANCE	ORF11.	TETM GENE.	LET 858.	SIMILARITY TO EGF-LIKE	NONMUSCLE MYOSIN HEAVY	NONMUSCLE MYOSIN HEAVY	NONMUSCLE MYOSIN HEAVY	DNA FOR DNAJ, COMPLETE	NONMUSCLE MYOSIN HEAVY	NONMUSCLE MYOSIN HEAVY	T24D5.1.	N-METHYL-D-ASPARTATE R	N-METHYL-D-ASPARTATE R	N-METHYL-D-ASPARTATE R	TRKB (FRAGMENT).	MYOSIN HEAVY CHAIN, NO .:	
018597	002606	Q18238	004393	022627	019671	039135	053770	607790	057224	047810	017336	018857	027991	012989	027990	033700	062707	062706	022732	012879	063728	008948	091373	002015	
m	σ.	<u>س</u>	œ	m	m	œ	<u>о</u>	11	о -	σ -	<u>ო</u>	m	4	7	4	ص -	10	10	m		10	10	12	12	
398	146	188	227	366	405	466	639	639	639	639	897	2946	66	106	109	157	272	282	304	1464	1464	1464	282	2007	
25.0	24.6	24.6	24.6	24.6	24.6	24.6	24.6	24.6	24.6	24.6	24.6	24.6	24.2	24.2	24.2	24.2	24.2	24.2	24.2	24.2	24.2	24.2	23.8	23.8	
64	63	63	63	63	63	63	63	63	63	63	63	63	62	62	62	62	62	62	62			62		61	
21	22	23	24	25	792	.27	28	29	30	31	32	33	34	35	36	37	38	39	0,7	41	42	43	44	45	

ALIGNMENTS

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RESULT ID 06 AC 06 DT 01 DT 01

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361 ECSCRELDEICRLY-LDHGALGARLTG 386
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                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                     01-JUL-1997 (TREMBLREL. 04,
01-JUL-1997 (TREMBLREL. 04,
01-JAN-1998 (TREMBLREL. 05,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 27.3%;
Best Local Similarity 48.1%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                          SIMILAR TO GALACTOKINASE.
                                                                                                                                                           01-JUL-1997 (TREMBLREL.
01-JUL-1997 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                          CAENORHABDITIS ELEGANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DYSTROPHIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 94150718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WATERSTON R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    og1493;
                                                                          RESULT 9
ID 001969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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PAITAN Y., BOULTON N., RON E., ROSENBERG E., ORR E.;
SUBMITTED (CCT-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CATALYTIC ACTIVITY: ATP-DEPENDENT BREAKAGE, PASSAGE AND REJOINING
                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POIRIER F., CHAN C.T.J., IIMMONS P., ROBERISON E.J., EVANS M.J., RIGBY P.W.J.; 19 DEVELOPMENW. 13:1105-1114(1991). EMBL: X58196; G51133; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                            ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ï
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 28.1%; Score 72; DB 10; Length 147; Best Local Similarity 32.1%; Pred. No. 3.94e-01; Matches 9; Conservative 9; Mismatches 10; Indels
                                                                                                                                                                        Length 1876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 72; DB 9; Length 815;
Pred. No. 3.94e-01;
2; Mismatches 6; Indels
                                                                                                                                                                 Query Match 28.5%; Score 73; DB 3; Length 1876
Best Local Similarity 41.7%; Pred. No. 2.65e-01;
Matches 10; Conservative 5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MYXOCOCCUS XANTHUS.
PROKARYOTA; GRACILICUTES; SCOTOBACTERIA; MYXOBACTERALES;
MYXOCOCCACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           061639
061639;
01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
J. BIOL. CHEM. 271:13892-13899(1996).
EMBL; U52192; G1272420; -.
FLYBASE; B407015278; P13K6B.
SEQUENCE 1876 AA; 210505 WW; DF107ECF CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OF DOUBLE-STRANDED DNA.
EMBL; AJ000543; E1168188; -.
PROSITE; PS00117; TOPOISOMERASE_II; 1.
SEQUERASE; TOPOISOMERASE_INDING.
SEQUENCE 815 AA; 89636 MW; 65A25520 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147 AA; 16309 MW; 6DC857F5 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           815 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 CCNONHYTTCLRNLLQGEAERTDGVNIL 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 CCRQKTCSCRLYELLHGAGNHAAGILTL 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                     501 RRKTCT-RLYELISDQRTDDPELL 523
                                                                                                                                                                                                                                                                                                                                                                     8 ROKICSCRLYELLHGAGNHAAGIL 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  691 PSCRRRSTWSCRLCAEHLRGAG 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 PDCCRQKTCSCRLY-ELLHGAG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 28.1%;
Best Local Similarity 59.1%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1998 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA GYRASE B SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 92249159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-C57B1/6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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GYRB.

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BONFIELD J., BURTON J., CONNELL M., COPER J., COULSON A.,
BONFIELD J., BURTON J., CONNELL M., COPER J., COULSON A.,
GARDNER A., GREEN P., HAWINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., CALLEGHAN M.,
PARSONS J., PERCY C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY MIEG J., THOMAS K., VANDIN M., VANGHAN R., WATERSTON R.,
WATURE 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                EUKARYOTA; METAZOA; ACOELOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
CHONDRICHTHYES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
m
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Pred. No. 8.65e-01;
4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL, AF003739, G2105488; --
PROSITE; PSO0627; GHMP KINASES_ATP; 1.
SEQUENCE 426 AA; 47290 MW; 7CBEF743 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATTUNG S., GOELA D., WILSON R.;
SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
                                                                CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RAVIN A.J., DYER S.M., YEADON J.E., BURDEN S.J.; J. PHYSIOGL, (PARIS) 0:131-133(1991).
EMED: M37645; G397971; -
PROSITE; PS01159; WW_DOMAIN_1; 1.
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MEDLINE, 92064638.
YEADON J.E., LIN H., DYER S.M., BURDEN S.J.;
J. CELL BIOL. 115:1069-1076(1991).
426 AA
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; ARTIODACTYLA.
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                                                                                                     Score 66; DB 9; Length 479;
Pred. No. 3.99e+00;
5; Mismatches 5; Indels
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STRAIN-168;
KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL, D50453; H050458; -
EMBL, 299106; E1182356; -
SEQUENCE 479 AA; 55166 MW; 3C2DIF5A CRC32;
                                                                                                                                                                                                                                            RESULT 15

1D 028584

AC 028584

AC 028584

O1-NOY-1996 (TREMBLREL. 01, CREATED)

01-NOY-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)

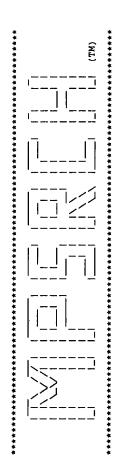
01-NOY-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)

DE KAP5.5 KERATIN PROTEIN (FRAGMENT).
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197 AA; 17474 MW; 731C19CA CRC32;
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TISSUE-WOOL FOLLICLE;
MEDLINE; 94358456.
JENKINS B.J., POWELL B.C.;
J. INVEST. DERMATOL. 103:310-317(1994).
EMBL; X73435; G313722; ...
KERATIN.
                                                                                                        Query Match
Best Local Similarity 41.2%;
Matches 7; Conservative
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Best Local Similarity 58.3%;
Matches 7; Conservative
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15 RLYELLHGAGNHAAGIL 31
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SEQUENCE
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Search completed: Thu Jul 30 09:21:29 1998 time: 17 secs.

87 VPVCCRVPACSC 98 :| | | | :| | 3 LPDCCRQKTCSC 14

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Thu Jul 30 09:20:12 1998; MasPar time 4.75 Seconds 253.613 Million cell updates/sec

>US-08-938-548A-8 (1-33) from US08938548A.pep 256 1 QPLPDCCRQKTCSCRLYELLHGAGNHAAGILTL 33 lar output not generated. Description: Perfect Score: Title:

Sequence:

PAM 150 Gap 11 Scoring table:

120441 seqs, 36531193 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d Database:

Mean 30.310; Variance 51.743; scale 0.586 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Pred. No.	9.01e-01	1.84e+00	2.63e+00	2.63e+00	3.73e+00	5.28e+00	5.28e+00	7.44e+00	7.44e+00	7.44e+00	1.05e+01	1.05e+01	1.05e+01	1.46e+01	1.46e + 01	1.46e+01	1.46e+01	1.46e+01	1.46e+01	1.46e+01	1.46e+01	1.46e+01	1.46e+01
	Description	hypothetical protein	dystrophin homolog -	oct2 protein isoform	sperm mitochondrial c	tetracycline-minocycl	Ig alpha chain C regi	Ig alpha chain C regi	UDPqlucose 4-epimeras	gene D3 protein - mou	transcriptional regul	hypothetical protein	keratin KAP5.5 - shee	beta-fructofuranosida	Omega-aga-1vb (nmr, m	Omega-aga-1vb (nmr, 2	omega-agatoxin-ivb -	omega-agatoxin IVB -	omega-agatoxin III, 8	omega-agatoxin IIIA -	omega-agatoxin III, 8	cell division protein	pigment deposition co	agout1 protein precur
	QI .	S24303	A41130	860079	A37199	JN0800	AHRB	S09276	S11223	156329	B69764	C64314	146413	S33920	10MB	10MA	1AGG	A44664	B54252	A42335	A54252	B64052	A46298	137143
	BB :	N	~	~	~	~	Н	~	~	~	~	~	~	~	'n	Ŋ	'n	Н	~	~	N	~	N	N
	Query Match Length DB	147	870	93	143	641	299	338	347	425	479	155	197	589	35	48	48	48	16	92	16	103	131	132
æ,	Query	28.1	27.3	27.0	27.0	26.6	26.2	26.2	25.8	25.8	25.8	25.4	25.4	25.4	25.0	25.0	25.0	25.0	25.0	25.0	25.0	25.0	25.0	25.0
	Score	72	70	69	69	89	67	67	99	99	99	65	65	65	64	64	64	64	64	64	64	64	64	64
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ALIGNMENTS

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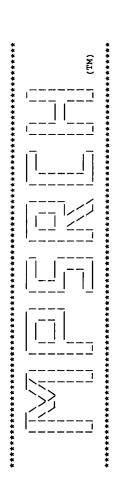
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CLASSIFICATION
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5-343
SUMMARY
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                                                   *superfamily immunoglobulin C region; immunoglobulin homology duplication; glycoprotein; heterotetramer; immunoglobulin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic Acids Res. (1990) 18:5289 CDNA from rat cells with reconstitutive galactose-epimerase activity in E. coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zeschnigk, M.; von Wilcken-Bergmann, B.; Starzinski-Powitz
stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger
                                                                                                                       #domain immunoglobulin homology #label IGG1\
#domain immunoglobulin homology #label IGG2\
#blnding_site carbohydrate (Asn) (covalent) #status
predicted
#length 299 #checksum 2361
                                                                                                                                                                                                                                                                                                                                                                                                                                Ig alpha chain C region - rabbit (fragment)
#formal_name Oryctolagus cuniculus #common_name domestic
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16-Aug-1996
S09276
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UDPgalactose 4-epimerase
#formal name Rattus norvegicus #common_name Norway rat
18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change
08-sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #authors Burnett, R.C.; Hanly, W.C.; Zhal, S.K.; Knight, K.L. #journal EMBO J. (1989) 8:4041-4047
#title The 19th heavy-chain gene family in rabbit: cloning and sequence analysis of 13 C-alpha genes.
#cross-references MUID:90076124
                                                                                                                                                                                                                                                                       ï
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Pred. No. 5.28e+00;
4; Mismatches 2; Indels
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Pred. No. 5.28e+00;
4; Mismatches 2; Indels
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llarity 50.0%; P
Conservative
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                                                                                                                                                                                                                                Query Match 26.2%;
Best Local Similarity 50.0%;
Matches 7; Conservative
                                    oligomers.
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2 PLPDCCRQKTC-SC 14
                                                                                                                                                                                                                                                                                                      44 PFPDCCPANSCCTC 57
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#title
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189-261
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Runst, F.; ogasawara, N.; Moszer, I.; Albertini, A.M.;
Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessleres, P.;
Bolothin, A.; Borchert, S.; Boriss, R.; Boursier, L.; Brans,
A.; Braun, M.; Brignell, S.(C.; Bron, S.; Brouillet, S.;
Choi, S.K.; Codail, J.J.; Connerton, I.F.; Cummings, N.J.;
Daniel, R.A.; Denizot, F.Devine, K.M.; Duesterhoeft, A.;
Ehrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J.;
Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fujita,
M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galleron, N.; Ghim,
S.Y.; Glaser, P.; Goffeau, A.; Golightly, E.J.; Grandi, G.;
Gulseppl, G.; Guy, B.J.; Haga, K.; Halech, J.; Harwood,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #authors Tannenbaum, C.S.; Major, J.; Ohmori, Y.; Hamilton, T.A.
#journal J. Leukoc. Biol. (1993) 53:563-568
#title A lipopolysaccharide-inducible macrophage gene (D3) is a new member of an interferon-inducible gene cluster and is selectively expressed in mononuclear phagocytes.
#across-references MUID:93274206
#accession 156329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene D3 protein - mouse
#formal_name Mus sp. #common_name mouse
26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
28-Feb-1997
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#formal_name Bacillus subtilis
05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
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UDPglucose 4-epimerase homology
                                                                                                                                                                                                                                                    #domain UDPglucose 4-epimerase homology #label [#length 347 #molecular-weight 38225 #checksum 6947
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                                                                                                                                                                                                                                                                                                                                              Score 66; DB 2; Length 347;
Pred. No. 7.44e+00;
4; Mismatches 2; Indels
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##residues 1-425 ##label RES
##cross-references GB:S62227; NID:g385702; PID:g385703
##residues 1-347 ##label ZES
##cross-references EMBL:X53949; NID:g57791; PID:g57792
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A69580
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#authors Yu, H.; Rosen, M.K.; Schreiber, S.L.
#submission submitted to the Brookhaven Protein Data Bank, September 1993
#cross-references PDB:10MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #authors Yu, H.; Rosen, M.K.; Schreiber, S.L.
#submission submitted to the Brookhaven Protein Data Bank, September 1993
#cross-references PDB:10MA
#domain signal sequence #status experimental #label SIG\
#product beta-fructofuranosidase #status experimental
#label MAT\
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                                                                                 #binding_site carbohydrate (Asn) (covalent) #status
predicted\
#binding_site phosphate (Thr) (covalent) #status
predicted\
#binding_site phosphate (Ser) (covalent) #status
predicted
#length 589 #molecular-weight 63650 #checksum 1032
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#disulfide_bonds
#length 35 #molecular-weight 3804 #checksum 7419
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Pred. No. 1.46e+01;
                                                                                                                                                                                                                       Query Match 25.4%; Score 65; DB 2; Lu
Best Local Similarity 42.1%; Pred. No. 1.05e+01;
Matches 8; Conservative 6; Mismatches 4
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Pred. No. 1.46e+
2; Mismatches
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#region turn (type II)\
#disulfide_bonds\
#disulfide_bonds\
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#region turn (type
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#disulfide_bonds\
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Best Local Similarity 45.5%;
                                                                                                                                                                                                                                                                                                               15 RLYELLHGAGNHAAGILTL 33
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25.0%;
Best Local Similarity 45.5%;
Matches 5; Conservative
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254,259,318,322,
388,463,518,527
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#submission
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24-589
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REFERENCE
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REFERENCE
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1-17
9-22
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SUMMARY
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TITLE
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        Matches
        5; Conservative
        2; Mismatches
        4; Indels
        0; Gaps
        0;

        Db
        19 CCRGRPCRCSM
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        11 : 1 : 1 : 0
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu Jul 30 09:21:47 1998; MasPar time 1.31 Seconds 147.949 Million cell updates/sec ular output not generated. ou:

>US-08-938-548A-8 (1-33) from USO8938548A.pep 256

1 QPLPDCCRQKTCSCRLYELLHGAGNHAAGILTL 33 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

63816 segs, 5850866 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

a-issued 1:5_COMB 2:PCT9_COMB 3:backfiles Database:

Mean 21.451; Variance 82.349; scale 0.260 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	2.23e+01	2.23e+01	2.23e+01	2.23e+01	2.23e+01	2.23e+01	3.29e+01	3.29e+01	4.83e+01	5.85e+01	5.85e+01	5.85e+01	5.85e+01	5.85e+01	7.08e+01	7.08e+01	8.55e+01	8.55e+01	8.55e+01	1.24e+02	1.24e+02	1.24e+02	1.24e+02
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Description	Seguence	Sequence	Patent No.	Sequence																			
QI	US-08-249-	-9E0-80-SD	PCT-US95-0	PCT-US94-0	us-08-469-	PCT-US95-0	US-08-485-	US-08-620-	US-08-026-	US-08-487-	US-08-480-	US-08-477-	US-08-137-	US-08-233-	5223425-6	US-08-279-	US-08-658-	us-08-296-	US-08-296-	US-08-019-	US-08-379-	US-08-121-	PCT-US94-1
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Length	39	39	39	39	39	348	1167	1168	1464	42	42	42	42	59	222	334	283	1019	1083	21	48	724	724
Query Match	25.8	25.8	25.8	25.8		25.8	25.0	25.0	24.2	23.8	23.8	23.8	23.8	23.8	23.4	23.4	23.0	23.0	23.0	22.3	22.3	22.3	22.3
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Gaps

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Sequence 40, Application US/08469569
Patent No. 5606032
GENERAL INFORMATION:
APPLICANT: Goodearl, Andrew; Stroobant, Paul;
APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
APPLICANT: Chen, Maio Su; Hiles, Ian
TITLE OF INVENTION: Glial Mitogenic Factors, Their
TITLE OF INVENTION: Preparation and Use
NUMBER OF SEQUENCES: 184
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                             Length 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39 AA
                                                                                                                                                                                                                                                                                                             Score 66; DB 2; L
Pred. No. 2.23e+01;
1; Mismatches 1
                REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 04585/028WO1
TELECOMMUTCATION INFORMATION:
TELEFHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEFAX: 200154
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/469,569
FILING DATE: 06-UN-1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/036,555
FILING DATE: 24-MAR-1993
APPLICATION NUMBER: 07/965,173
FILING DATE: 23-CCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/965,173
FILING DATE: 03-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 03-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/907,138
FILING DATE: 30-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/863,703
FILING DATE: 03-APRIL-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 40, Application US/08469569
                                                                                                                                                                                                                                                  TOPOLOGY: linear
KCE 39 AA; 3760 MW; 6521 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
NAME: Clark, Paul T.
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 03-APRI PRIOR APPLICATION DATA:
                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                             8 CCR-TICACR 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-469-569-40
                                                                                                                                                                                                                                                                     SEQUENCE
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ID US
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GENERAL INFORMATION:
APPLICANT: Robert Sklar, Mark Marchionni,
APPLICANT: David I. Gwynne
TITLE OF INVENTION: METHODS FOR ALTERING
TITLE OF INVENTION: MUSCLE CONDITION
NUMBER OF SEQUENCES: 185
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 66; DB 2; L
Pred. No. 2.23e+01;
1; Mismatches 1
                                                                                                                                                                                                                           NAME: Hanson, Norman D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5250.5
TELECOMUNICATION INFORMATION:
TELECHONE: (212) 688-9200
TELEFRAY: (212) 688-9200
ITELEFRAY: (212) 838-3884
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
                                                                     PRIOR APPLICATION DATE:
APPLICATION NUMBER: 07/863,703
FILING DATE: 03.APRIL-1992
PRIOR APPLICATION DATE: 0.8.91
APPLICATION NUMBER: U.K. 91 07566.3
FILING DATE: 10.APRIL-1991
ATTORNAY AGENT INFORMATION:
NAME: HANSON, NORMAN D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360
MEDIUM TYPE: kb storage
COMPUTER: IBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SIGNEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCI/US94/05083C
FILING DATE: 06-MAY-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209, 204
FILING DATE: 08-MAR-94
PRIOR APPLICATION DATA:
FILING DATE: 06-MAY-93
FILING DATE: 06-MAY-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 40, Application PC/TUS9405083C
                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/907,138
FILING DATE: 30-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
CE 39 AA; 3760 MW; 6521 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
  FILING DATE: 03-SEP-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Boston
STATE: Massachusetts
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.8%;
Similarity 70.0%;
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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RESULT

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Best Loca Matches

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Gaps

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3; Indels

Length 1168;

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Sequence 1, Application US/08026138E
Patent No. 5502166
GENERAL INFORMATION:
APPLICANT: Masayoshi MISHINA
TITLE OF INVENTION: NOVEL PROTEINS AND GENES CODING THE SAME
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSE: Nishiohata Residence 1-107
STREET: 5214, Nishiohata-machi
CITY: Niigata-shi
STATE: Niigata-ken
COUNTRY: JAPAN
ZIP: 951
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS V.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE: NOVEL PROTEINS AND GENES CODING THE SAME RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 to 1464 RC 1464 AA; 165489 MW; 11224000 CN;
                                                                                                                                                                                                                                                                                       1464 AA
                                                                Score 64; DB 1; L
Pred. No. 3.29e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 26-FEB-1993

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

PAPLICATION NUMBER: 10 39563/1992

FILING DATE: 30-JWN-1992

APPLICATION NUMBER: JP 215017/1992

FILING DATE: 30-JWN-1992

APPLICATION NUMBER: JP 215017/1992

FILING DATE: 13-NOV-1992

APPLICATION NUMBER: JP 303878/1992

FILING DATE: 13-NOV-1992

ATTORNEY, AGENT INFORMATION:

NAME: Hamburg, C.Bruce

REGISTRATION NUMBER: 22,389

REFERENCE/DOCKET NUMBER: 22,389

REFERENCE/DOCKET NUMBER: T-4551

TELEPHONE: (212) 986-2340

TELEPHONE: (212) 986-2340
                                                                                                               3; Mismatches
INDIVIDUAL ISOLATE: 167p
SEQUENCE 1168 AA; 131542 MW; 7175894 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/026,138E
FILING DATE: 26-FEB-1993
                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: mouse
TISSUE TYPE: cerebellum
PUBLICATION INFORMATION:
AUTHORS: Masayoshi MISHINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1464 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                       STANDARD;
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                                                              y Match
Local Similarity 45.5%;
hes 5; Conservative
                                                                                                                                                     873 PNCCKPAACQC 883
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ID US-08-026-138E-1
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Sequence 1, Applic
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TITLE OF INVENAT
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TITLE OF INVENA
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Patent No. 5670365
GENERAL INFORMATION
APPLICANT: Feitelson, Jerald S.
TITLE OF INVENTION: Identification of, and Uses For, Nematicidal
TITLE OF INVENTION: Bacillus thuringiensis Genes, Toxins, and Isolates
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
                                                                                                                                                                                                                                                                                                                               ö
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Pred. No. 3.29e+01;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1168 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Plorida
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/540,104
FILING DATE: 06-0CT-1995
CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
                                                                                                                                                                                                                    MOLECULE TYPE: protein
FENCE 1167 AA; 131657 MW; 7095219 CN;
  REFERENCE/DOCKET NUMBER: MA48DD2.C1 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/620,717A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: MA94.C1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9, Application US/08620717A
                                        TELEPHONE: (904) 375-8100
INFORMATION FOR SEQ ID NO: 6: SEGUENCE CHARACTERISTICS:
LENGTH: 1167 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEO ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1168 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 45.5%;
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                       873 PNCCKPAACQC 883
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                                                                                                                                                                                                                                            SEQUENCE
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RESULT
ID US
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PRT;

STANDARD;

US-08-477-383-23

RESULT

XXXXXX

Sequence 23, Application US/08477383 Patent No. 5589340 GENERAL INFORMATION: APPLICANT: Olivera, Baldomero M.

COUNTRY: U.S.A. ZIP: 20005

Sequence 23, Application US/08477383

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Sequence 23, Application US/08137800
Patent No. 5514774
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: McIncosh, J. Michael
APPLICANT: McIncosh, J. Michael
APPLICANT: McIncosh, J. Michael
APPLICANT: McIncosh, J. Michael
APPLICANT: Santos, Ameurfina D.
TITLE OF INFORTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS: 53
CORRESPONDENCE ADDRESS: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue N.W., Suite 1000
CITY: Washington
STATE: DC
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: NACHORIGETES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Indels
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Pred, No. 5.85e+01;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,800
FILING DATE: 19-COT-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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APPLICANT: DOTAN, James L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 51, Application US/08233788A
                                                                               Sequence 23, Application US/08137800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Conus ochroleucus
SEQUENCE 42 AA; 4618 MW; 9505 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Ihnen, Jeffrey L. REGISTRATION NUMBER: 28,957 REFERENCE/DOCKET NUMBER: 24, TELECOMMUNICATION INFORMATION: 202-962-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPAX: 202-902 UNIVERSITION FOR SEQ ID NO: 23 SEQUENCE CHARACTERISTICS: "PUCTH: 42 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 23.8%;
Best Local Similarity 47.4%;
Matches 9; Conservative
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MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
OPERATING SYZENE: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,383
FILING APPLICATION DATA:
APPLICATION NUMBER: US/08/477,383
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/137,800
FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/48/8
FILING DATE: 29-JUN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STRATE: DC
                                      42 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-107673
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
                                                                                                                                                                                                                                                                                                  APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: Macintosh, J. Michael
APPLICANT: Santos, Ameurfino S.
TITLE OF INVENTION: Conctoxin Peptides
NUMBER OF SEQUENCES: 59
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Gaps

Score 61; I Pred. No. 5.

23.8%; llarity 47.4%; Conservative

Query Match Best Local Similarity Matches 9; Conserv

ORIGINAL SOURCE: ORGANISM: Conus ochroleucus JENCE 42 AA; 4618 MW; 9505 CN;

SEQUENCE

TOPOLOGY: linear MOLECULE TYPE: peptide HYPOTHETICAL: NO

LENGIH: 42 amino acids

TYPE: amino acid STRANDEDNESS:

202-962-8300

TELEFAX:

INFORMATION FOR SEQ ID NO

PRT;

STANDARD;

LT 13 US-08-137-800-23

RESULT ID US

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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu Jul 30 09:19:34 1998; MasPar time 3.95 Seconds 128.266 Million cell updates/sec ular output not generated. : 0

>US-08-938-548A-8 (1-33) from USO8938548A.pep 256 1 QPLPDCCRQKTCSCRLYELLHGAGNHAAGILTL 33 Description: Perfect Score:

PAM 150 Scoring table: Sequence:

Gap 11

Searched:

124785 seqs, 15338987 residues

Minimum Match 0% Listing first 45 summaries Post-processing:

Journal 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 4:part14 15:part15 16:part16 17:part17 18:part18 9:part18 20:part20 21:part21 22:part22 23:part22 23:part25 26:part26 27:part27 a-geneseq31-2 Database:

Mean 22.991; Variance 84.736; scale 0.271 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

Score Match Length DB ID Description Fred. 1363 23 W12414 Porcine complement in 6.266 75 29.3 373 18 K98461 Murine IEC-ed-3 homo 9.466 25.8 102 1 P95679 Kenopus Vgl protein f. 206 25.8 102 1 P95679 Xenopus Vgl protein f. 206 25.8 102 1 P95679 Xenopus Vgl protein f. 5.806 25.8 102 1 P95679 Xenopus Vgl protein f. 5.806 25.8 102 1 P95679 Xenopus Vgl protein f. 5.806 25.4 78 5 P20020 Sequence of a foot an 7.066 4 25.0 45 23 W10106 Human agouti signall 8.596 4 25.0 48 11 R60293 Calcium channel inhib 8.596 4 25.0 48 11 R60293 Calcium channel inhib 8.596 64 25.0 130 23 W10101 Murine agouti signall 8.596 64 25.0 130 23 W10101 Murine agouti signall 8.596 64 25.0 130 23 W10101 Murine agouti signall 8.596 64 25.0 130 23 W10101 Murine agouti signall 8.596 64 25.0 130 23 W10101 Murine agouti signall 8.596 64 25.0 1167 27 W31504 Human agouti signall 8.596 64 25.0 1167 27 W31504 Human agouti signall 8.596 64 25.0 1167 27 W31504 Human agouti signall 8.596 64 25.0 1168 23 W16326 Human WMDA R2A recept 1.276 224.2 1464 10 R55299 Human MDA R2A recept 1.277			æ			COTTANADA		
Match Length DB ID Description 30.1 363 23 W12414 Porcine complement in 29.3 373 18 R98461 Murine ICE-ced-3 homo 27.0 329 26 W29877 Murine ICE-ced-3 homo 27.0 329 26 W29877 Jysophosphatidic acid 25.8 102 1 P95679 Xenopus Vgl protein f 25.8 48 20 W01619 Human uridine diphosp 25.4 78 5 P20020 Sequence of a foot an 25.0 45 23 W10105 Murine agouti signall 25.0 48 9 R45611 AG1 toxin. 25.0 48 11 R60293 Calcium channel inhib 25.0 180 23 W10102 Human agouti signall 25.0 130 23 W10102 Human agouti signall 25.0 1167 20 W1053 Bacillus thuringiensi 25.0 1167 20 W1053 Bacillus thuringiensi 25.0 1167 20 W1053 Human agouti signall 25.0 1167 20 W1053 Human WDA R2A recept			Query					
363 23 W12414 Porcine complement in 373 18 R98461 Murine Interleukin-1 329 26 W2987 Lysophosphatidic acid 202 195679 Lysophosphatidic acid 202 1 P95679 Lysophosphatidic acid 203 248 20 W01619 Human uridine diphosp 28 P20020 Sequence of a foot an 45 23 W10106 Murine agouti signall 48 9 R45611 AGI toxin. 48 11 R60293 Calcium channel inhib 48 1 R60293 A. aperta venom fract 130 23 W10102 Human agouti signall 1167 20 W10653 Murine Agouti Starakine 167 20 W10653 Murine Agouti Starakine 167 20 W10654 Tecept 40 W1085529 Human NWDA R2A recept	ι Ν	ore	Match	Length		ar E	Description	Pred. No.
373 18 R98461 Murine ICE-ced-3 homo 373 13 R66767 Murine interleukin-1 372 6 W2987 Lysophosphatidic acid 102 1 P95679 Kaopus Vgl protein f As 20 W01619 Kaopus Vgl protein f As 20 W01619 Sequence of a foot an 45 23 W10106 Human uridine diphosp R5 23 W10106 Human agouti signall As 23 W10105 Murine agouti signall As 11 R60293 Calcium channel inhib 48 11 R60293 Calcium channel inhib 48 R44209 A. aperta venom fract 130 23 W10101 Murine agouti signall 1115 27 W31504 Numan agouti signall 1167 20 W1053 Bacillus thuringiensi 1168 23 W16326 Human NWDA R2A recept 144 10 R55529 Human NWDA R2A recept		77	30.1	363	23	W12414	Porcine complement in	6.26e+00
373 13 R66767 Murine interleukin-1 329 6 W29877 Lysophosphatidic acid 102 1 P95679 Kenpous Vg1 protein f 78 20 W01619 Human uridine diphosp 78 5 P20020 Sequence of a foot an 45 23 W10106 Human agouti signall 48 R44209 A. aperta venom fract 130 23 W10102 Human agouti signall 131 23 W10101 Murine agouti signall 131 23 W10101 Murine agouti signall 130 23 W10101 Murine agouti signall 1167 20 W1054 Nematodial toxin 167 P 1167 20 W1055 Bacillus thuringians 1168 23 W16326 Human WMAR R2A recept 144 10 R55599 Human NWAR R2A recept		75	29.3	373	18	R98461	Murine ICE-ced-3 homo	9.46e+00
329 26 W29877 Lysophosphatidic acid 328 20 W01619 Earnors Ydl protein f 348 20 W01619 Human uridine diphosp 78 5 P20020 Sequence of a foot an 45 23 W10106 Human agouti signalli 48 9 R45611 AGI toxin. 48 9 R44209 A. aperta venom fract 130 23 W10101 Human agouti signalli 131 23 W10102 Human agouti signalli 131 23 W10101 Human agouti signalli 1167 20 W10653 Bacillus thuringiensi 1168 23 W16326 Nematocidal toxin 167 31 0 R5529 Human NWDA R2A recept		75	29.3	373	13	R66767	Murine interleukin-1	9.46e+00
102 1 P95679 Xenopus Vg1 protein f 348 0 W01619 Human uridine diphosp 78 22 W10166 Human uridine diphosp P20020 Sequence of a foot an 45 23 W10106 Human agouti signalli 48 1 R60293 Calcium channel inhib 48 R44209 A. aperta venom fract 130 23 W10102 Human agouti signalli 1167 27 W31504 Nematode toxin 167P p 1167 20 W1053 Bacillus thuringiensi 1168 23 W16326 Human WMDA R2A recept 1464 10 R55529 Human NWDA R2A recept		69	27.0	329	56	W29877	Lysophosphatidic acid	3.20e+01
348 20 W01619 Human uridine diphosp 78 5 P20020 Sequence of a foot an 45 23 W10106 Human agouti signall 48 8 R45611 AG1 toxin. 48 1 R60293 Calcium channel inhib 48 8 R44209 A. aperta venom fract 130 23 W10102 Human agouti signall 131 23 W10101 Murine agouti signall 1167 20 W1053 Nematode toxin 167 P p 1167 20 W1053 Nematodial toxin 167 P 1168 23 W16326 Human NWDA R2A recept 1464 10 R55599 Human NWDA R2A recept		99	25.8	102	-	P95679	Xenopus Vq1 protein f	5.80e+01
78 5 P20020 Sequence of a foot an 45 23 W10106 Human agouti signall 45 23 W10106 Murine agouti signall 48 9 R45611 AGI toxin. 48 9 R45613 Calcium channel inhib 48 11 R60293 Calcium channel inhib 48 R44209 A. aperta venom fract 130 23 W10102 Human agouti signall 1167 27 W31504 Nematode toxin 167 p 1167 20 W10653 Bacillus thuringiensi 1168 23 W16326 Nematocidal toxin 167 34 O R55508 Tarantula spider veno 1464 10 R55529 Human NWDA R2A recept		99	25.8	348	20	W01619	Human uridine diphosp	5.80e+01
45 23 W10106 Human agouti signalli 48 19 R45611 AGI toxin. 48 11 R60293 Calcium channel inhib 48 R44209 A. aperta venom fract 130 23 W10102 Human agouti signalli 131 23 W10101 Murine agouti signalli 1167 20 W10653 Bacillus thuringiensi 1168 23 W16326 Nematocidal toxin 167 p 1168 23 W16326 Human NWDA R2A recept 1464 10 R55529 Human NWDA R2A recept		65	25.4	78	Ŋ	P20020	Sequence of a foot an	7.06e+01
45 23 W10105 Murine agouti signall 48 11 R60293 Calcium channel inhib 48 R44209 A. aperta venom fract 130 23 W10102 Human agouti signall 1157 27 W31504 Nematode toxin 157 P 1167 20 W1053 Bacillus thuringiensi 1168 23 W16326 Mematocidal toxin 167 P 1168 23 W16326 Human NWDA R2A recept 1464 10 R55529 Human NWDA R2A recept		64	25.0	45	23	W10106		8.59e+01
48 9 R45611 AG1 toxin. 48 11 R60293 Calctum channel inhib 48 18 R44209 A. aperta venom fract 130 23 W10102 Human agouti signall 131 23 W10101 Murine agouti signall 1167 27 W31504 Nematode toxin 167 p 1167 20 W10553 Bacillus thuringiensi 1168 23 W16326 Nematocidal toxin 167 134 10 R55599 Human NWDA R2A recept		64	25.0	45	23	W10105	Murine agout1 signall	8.59e+01
48 11 R60293 Calcium channel inhib 48 R44209 A. aperta venom fract 130 23 W10102 Human agouti signall 131 23 W10101 Murine agouti signall 1167 27 W31504 Nematode toxin 167 P 1167 20 W10653 Bacillus thuringiensi 1168 23 W16326 Nematocidal toxin 167 34 10 R55508 Tarantula spider veno 1464 10 R55529 Human NWDA R2A recept		64	25.0	48	σ	R45611	AG1 toxin.	8.59e+01
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130 23 W10102 Human agouti signalli 131 34 W10101 Murine agouti signalli 1167 27 W31504 Nematode toxin 167P p 1167 20 W10553 Bacillus thuringiensi 1168 23 W16326 Nematocidal toxin 167 at 10 R55088 Tarantula spider veno 134 10 R55529 Human NWDA R2A recept		64	25.0	48	œ	R44209	A. aperta venom fract	8.59e+01
131 23 W10101 Murine agouti signall 1167 27 W31504 Nematode toxin 167P p 1167 20 W10653 Bacillus thuringiensi 1168 23 W16326 Nematocidal toxin 167 34 10 R55088 Tarantula spider veno 1464 10 R55529 Human NMDA R2A recept		64	25.0	130	23	W10102	Human agouti siqualli	8.59e+01
1167 27 W31504 Nematode toxin 167P p 1167 20 W10653 Bacillus thuringiensi 1168 23 W16326 Nematocidal toxin 167 34 10 R55088 Tarantula spider veno 1464 10 R55529 Human NWDA R2A recept		64	25.0	131	23	W10101	Murine agout1 signall	8.59e+01
1167 20 W10653 Bacillus thuringiensi 1168 23 W16326 Nematocidal toxin 167 134 10 R55088 Tarantula spider veno 1464 10 R55529 Human NWDA R2A recept		64	25.0	1167	27	W31504	Nematode toxin 167P p	8.59e+01
1168 23 W16326 Nematocidal toxin 167 134 10 R55508 Tarantula spider veno 1464 10 R55529 Human NWIA R2A recept		64	25.0	1167	20	W10653	Bacillus thuringiensi	8.59e+01
.2 34 10 R55088 Tarantula spider veno .2 1464 10 R55529 Human NMDA R2A recept .		64	25.0	1168	23	W16326	Nematocidal toxin 167	8.59e+01
10 R55529 Human NMDA R2A recept		62	24.2	34	ព	R55088	Tarantula spider veno	1.27e+02
		62	24.2	1464	ព	R55529	Human NMDA R2A recept	1.27e+02

1.27e+02 1.27e+02 1.27e+02 1.27e+02 1.53e+02 1.53e+02 1.53e+02 1.53e+02 1.53e+02 1.53e+02 1.53e+02 1.86e+02 1.86e+02 1.86e+02 1.86e+02 2.24e+02 2.24e+02 2.24e+02	
Human N-methyl-D-aspa Human excitatory amin Glutamic acid recepto Rat NWDA receptor sub A-lineage conotoxin p predatory cone snall Salmonella enteritidi Human membrane antige TctA sequence. Human bg protein asso Human bg protein asso Gyn d allergen Bl. Cherry polyphenol oxi E. coli DNA polymeras DNA polymerase III ho APP-HCV-EZ fusion pro Spider venom peptide N-terminal sequence o Funnel web spider ven Connexin-32.	Sequence of viper ven Sequence of viper ven Ovine FSH beta subuni Ikaros protein. Mouse 22B/30B (candid Murine Lystl long iso
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R66039 R80970 R441952 W12745 W12745 W24890 W27333 W27333 W27333 W27333 W2735 W27333 W2733 W2	P91100 P91095 R10038 R92020 W31948
112 118 118 119 110 110 110 110 110 110 110 110 110	3 7 7 7 7 7 7 7 7
	129 129 334 3788 3788
44444888888884444440000	222 7.222 7.222 7.222 7.222 7.222
000000000000000000000000000000000000000	202222
0122222222222 0112E42862222222222222222222222222222222222	444444444444444444444444444444444444

ALIGNMENTS

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DNA encoding porcine complement inhibitor - useful in porcine organ transplant to humans claims are 12-14; 20pp; Japanese.

This protein is a porcine complement inhibitor encoded by pMCPcDNA (761098). The DNA is useful for large scale production of recombinant porcine complement inhibitor, which is useful for porcine organ transplantation into humans. The DNA clone pMCPcDNA is also useful in the analysis of the promoter region of porcine complement inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ï
                             24-SEP-1997 (first entry)
Porcine complement inhibitor.
porcine; pig; complement; inhibitor; organ transplantation; analysis; promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LT 2
R98461 standard; Protein; 373 AA.
R98461; 25-SEP-1996 (first entry)
Murine ICE-ced-3 homologue.
mIch-2; murine ICE-ced-3 homologue; programmed cell death;
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 77; DB 23; Length 363;
Pred. No. 6.26e+00;
7; Mismatches 9; Indels
                                                                                                                                                                                                   Murakami H, Shigehisa T, Toyomura K;
WPI; 97-087378/08.
N-PSDB; T61098.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98 plqeacrrkacs-nlpdplngqvsypng 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 PLPDCCROKTCSCRLYELLHGAGNHAAG 29
standard; Protein; 363 AA.
                                                                                                                    09-JAN-1997.
19-JUN-1996; J01704.
20-JUN-1995; JP-178254.
(NIME-) NIPPON MEAT PACKERS INC.
(NIHA-) NIPPON HAM KK.
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 30.1%;
Best Local Similarity 39.3%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          363 AA;
                                                                                          Sus scrofa.
WO9700951-A1.
                                                                                                                                                                                                                                                                                                                                                                                             Sequence
 W12414
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Hearing VJ:

WPI: 97-087323/08.

WPI: 97-087323/08.

New agouti signal protein peptide(s) and nucleic acids - used for altering melanin prodn., for treating e.g. melasma photo-ageing spots, solar keratosis or vitiligo

Talian 10; Page 11; 67pp; English.

The sequences given in W10101-29 are biologically active peptides

The sequences given in W10101-29 are useful for cosmetic purposes and fragments of the agouti signalling protein (ASP) which have depigmenting activity. These peptides are useful for cosmetic purposes and for clinical application in the prevention or treatment of various hyperpigmentary conditions and diseases such as melasma photoageing spots, solar keratosis, and post-inflammatory hyperpigmentation such as occurs at sites of wound healing. They can also be used to provide enhanced eumelanogenesis for treating eg. vitiligo, leucoderma, some forms of albinism and hair greying.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-529-1997 (first entry)
Human agout1 signalling protein fragment #2.
Agout1 signalling protein, ASP; depigmenting activity; cosmetic;
hyperpigmentary condition; melasma photoageing spots; solar keratosis;
post-inflammatory hyperpigmentation; wound healing; eumelanogenesis;
vitiligo; leucoderma; albinism; hair greying.
                                                                                                                              DNA corresp. to (part of) foot and mouth disease virus RNA - useful in prepn. of vaccines for producing antibodies against the virus Example; Fig 6; 57pp; English.

The inventors claim a DNA molecule comprising a nucleotide sequence corresp. to all or a portion of foot-and-mouth disease virus RNA (FMDV). The DNA molecule is esp. for a precursor of FMDV capsid protein. It esp. codes for FMDV protein p88 and VPI-VP4. It may code for very vy2 or vy4, vP2, vP3 and VPI contiguously. The inventors also claim a vaccine for stiumlating prodn. of antibodies against FMDV in a mammal which comprises at least one of the above recombinant proteins produced by a host cell transformed with the DNA.
  (NATR ) National Res Dev Corp. (WELL) Wellcome Foundation Ltd. Boothroyd JC, Cross GAM, Highfield PE, Winther MD, Rowlands DJ, Brown F, Harris TJK, Lowe PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 64; DB 23; Leuy ...
Pred. No. 8.59e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 65; DB 5; Length 78; Pred. No. 7.06e+01; 9; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-JAN-1997.
21-JUN-1996; U10695.
23-JUN-1995; US-000436.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 OKTCSCRLYELLHGAGNHAAGILT 32
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W10105 standard; protein; 45 AA.
W10105;
17-SEP-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45 qntcsthtyqglhst-thstlvls 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š.
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Best Local Similarity 37.5%;
Matches 9; Conservative
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Similarity 41.2%;
7; Conservative
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                                                                                        WPI; 82-26702E/14.
N-PSDB; N20019.
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WO9700892-A2.
                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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       anomalies, induction
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congenital craniofacial and other skeletal or dental anomalies, inductic of local endochondral bone formation in non-union fractures, peridontal applens. requiring bone formation and cartilage repair, eg in the treatment of osteoarthritis.

See also P95679-P95692 and N95097.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  In the treatment and diagnosis of galactosaemia claim 1; Page 43-44; 59pp; English.

Human mature uridine diphosphate galactose-4-epimerase (UDP-G4E)

(W01619) catalyses a reversible reaction between UDP-glucose and UDP-galactose that allows galactose residues to enter into the main pathways of glucose metabolism. A deficiency of the enzyme results from a CDNA clone (T58301) derived from a human endometrial tumour library. Recombinant UDP-G4E polypeptides can be produced in transformed host (e.g. E. coli, COS, Sf9 insect) cells or expressed in vivo for use in the treatment of UDP-G4E deficiency, e.g.
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                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                           W01619;
24-APR-1997 (first entry)
Human uridine diphosphate galactose-4-epimerase.
Uridine diphosphite galactose-4-epimerase; UDP-G4E; galactosaemia;
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Pred. No. 5.80e+01;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-AUG-1992 (first entry)
Sequence of a foot and mouth disease virus capsid protein encoded by a region of recombinant plasmid pFA61/t/6
Voctine; antibody; capsid protein; immunogen; antigen; foot and mouth disease.
Foot and mouth disease virus.
                                                                                                                                                            Length 102;
                                                                                                                                                                                                         2; Indels
                                                                                                                                                            Score 66; DB 1; Le
Pred. No. 5.80e+01;
4; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                   JT 6
W01619 standard; Protein; 348 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P20020 standard; Protein; 78 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-NOV-1996.
11-MAY-1995, U05785.
11-MAY-1995, WO-U05785.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25.8%;
53.8%;
                                                                                                                                                            Query Match 25.8%;
Best Local Similarity 56.3%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                     34 cpyplyeilngs-nha 48
                                                                                                                                                                                                                                                                            12 CSCRLYELLHGAGNHA 27
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GB-034130.
GB-038147.
GB-011064.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262 cgcriynlgtgtg 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ji H, Rosen CA;
WPI; 96-518666/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               348 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; T58301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
W09635778-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            galactosaemia.
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22-OCT-1980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-MAR-1982.
17-SEP-1981.
                                                                                                                Sequence
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Bacillus thuringlensis toxin gene - useful in recombinant hosts, particularly plants for the control of nematodes Claim 4; Page 35-39; 44pp; English.

This sequence represents the protein encoded by a polynucleotide of the invention. The polynucleotide of the invention is a sequence from a Bacillus thuringlensis (Bt) isolate selected from PS80JJ1, PS158D5, PS169E, PS177F1, PS1776, PS204G4 and PS204G6, that encodes a toxin active against nematodes. This sequence represents the 167P protein, and is a delta-endotoxin protein. The polynucleotides and toxins can be used for the control of nematode pests such as Panagrellus
                                                                                                                                                                                                                                                                                                                                                                                                                                                           New agouti signal protein peptide(s) and nucleic acids - used for altering melanin prodn., for treating e.g. melasma photo-ageing spots, solar keratosis or vitilido
claim 5; Page 8-9; 67pp; English
The sequences given in W10101-29 are biologically active peptides and fragments of the agouti signalling protein (ASP) which have depigmenting activity. These peptides are useful for cosmetic purposes and for clinical application in the prevention or treatment of various hyperpigmentary conditions and diseases such as melasma photoageing spots, solar keratosis, and post-inflammatory hyperpigmentation such as occurs at sites of wound healing. They can also be used to provide enhanced emmelanogenesis for treating eg. vitiligo, leucoderma, some forms of albinism and hair greying.
         Agouti signalling protein; ASP; depigmenting activity; cosmetic; hyperpigmentary condition; melasma photoageing spots; solar keratosis; post-inflammatory hyperpigmentation; wound healing; eumelanogenesis; vitiligo; leucoderma; albinism; hair greying.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-APR-1998 (first entry)
Nematode toxin 167P protein.
PCR primer; amplify; nematode toxic protein; Bacillus thuringiensis; delta-endotoxin gene; nematode pest control; Panagrellus redivivus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 64; DB 23; Leuy...
Pred. No. 8.59e+01;
......tches 6; Indels
                                                                                                                                                                                                                                                                          /note= "Start of Cysteine-rich motif"
                                                                                                                                                                                                                            /note= "Start of basic region"
                                                                                                                                                       /note= "Signal sequence"
32
                                                                                                                                                                                                                                                                                                                                                                     23-JUN-1995; US-000436.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; Protein; 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 41.2%;
Matches 7; Conservative
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Fu J, Narva KE, Payne J;
WPI; 97-480163/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-SEP-1997.
21-MAR-1997; U04755.
21-MAR-1996; US-590554.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167P protein.
Bacillus thuringiensis.
WO9734926-A2.
                                                                                                                                                                                                                                                                                                                                     21-JUN-1996; U10695
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                                                                                                                                                                                                                                                                                                                                                                                                                    Hearing VJ;
WPI; 97-087323/08.
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W31504 St
W31504;
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New agouti signal protein peptide(s) and nucleic acids - used for latering methanin prodn., for treating e.g. melasma photo-ageing spots, solar keratosis or vitiligo claim 6; Page 8-9; 67pp; English.

The sequences given in W10101-29 are biologically active peptides and fragments of the agouti signalling protein (ASP) which have depigmenting activity. These peptides are useful for cosmetic purposes and for clinical application in the prevention or treatment of various hyperpygmentary conditions and diseases such as melasma photoageing spots, solar keratosis, and post-inflammatory hyperpigmentation such as occurs at sites of wound healing. They can also be used to provide the performance of the provide station of the prevention of the provide stations and post-inflammatory hyperpigmentation such as course at sites of wound healing. They can also be used to provide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    solar keratosis;
Example; Page 17; 28pp; English.

The sequence is that of a polypeptide present in fraction K of the venom of Agelenopsis aperta, it blocks calcium channels in cells of both mammals and invertebrates, partic. those affecting neuronal and muscle cells. It may be used in the treatment of angina, hypertension, cardiomyopathies, supraventricular arrhythmia, cesophogeal achalasia, premature labour, and Raynaud's disease. It may also be of use in the study of cell physiology and in the control of invertebrate pests. It may be produced synthetically.
                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-SEP-1997 (first entry)

Human agouti signalling protein.

Agouti signalling protein. ASP; depigmenting activity; cosmetic;

Agouti signalling protein; melasma photoageing spots; solar Keratosi
phyperpigmentary condition; melasma photoageing spots; solar Keratosi
post-inflammatory hyperpigmentation; wound healing; eumelanogenesis;
vitiligo; leucoderma; albinism; hair greying.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Pred. No. 8.59e+01;
3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                          Length 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Start of Cysteine-rich motif"
                                                                                                                                                                                                                                                                        Score 64; DB 8; Lv
Pred. No. 8.59e+01;
2; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Start of basic region"
86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1..21
/note= "Signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  forms of albinism and hair greying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JT 13
W10102 standard; protein; 130 AA.
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W10101 standard; protein; 131 AA.
W10101;
17-SEP-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-SEP-1997 (first entry)
Murine agouti signalling protein.
                                                                                                                                                                                                                                                                        Query Match 25.0%;
Best Local Similarity 45.5%;
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23-JUN-1995; US-000436.
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Gaps

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protein - protein database search, using Smith-Waterman algorithm MPsrch pp

Thu Jul 30 09:17:23 1998; MasPar time 9.36 Seconds 584.625 Million cell updates/sec ular output not generated. on:

Title:

>US-08-938-548A-6 (1-130) from USO8938548A.pep 954 1 MNLPSTKVPWAAVTLLLLLL......GRRCPTATATALAPRGGSRV 130 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

Minimum Match 0% Listing first 45 summaries

140542 seqs, 42109429 residues

Searched:

Post-processing:

Database:

sptrembl5
1:sp_fung1 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_hubc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Mean 39.989; Variance 88.114; scale 0.454 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

3.56e-02	8.61e-02	3.65e-01	3.65e-01	1.95e+00	2.56e+00	2.56e+00	2.56e+00	3.36e+00	4.40e+00	4.40e+00	4.40e+00	4.40e+00	5.75e+00	5.75e+00	7.50e+00	7.50e+00	7.50e+00	7.50e+00	7.50e+00
HYPOTHETICAL 74.6 KD P	PLATELET GLYCOPROTEIN	ACYLOXYACYL HYDROLASE.	FRIZZLED PROTEIN HOMOL	PROLINE - AND LEUCINE-R	LECITHIN: CHOLESTEROL A	CYCLOOXYGENASE 1.	CYCLOOXYGENASE ISOFORM	SORTILIN PRECURSOR.	COLIA1 AND PDGFB FUSIO	C-SIS PROTO-ONCOGENE (LEUCINE ZIPPER WITH BA	PROSTAGLANDIN H SYNTHA	HYPOTHETICAL 23.1 KD P	TIGHT JUNCTION PROTEIN		POLYPROTEIN PRECURSOR	DNA BINDING PROTEIN E1	PROSTAGLANDIN ENDOPERO	SIMILARITY TO MOUSE SM
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74.6 KD P 3 10.8 567 10 008770 PLATELET GLYCOPROTEIN 8 10.3 574 10 008463 FRIZZLED PROTEIN HOMOL 3 9.6 106 8 Q41051 PROLINE-AND LEGGINE-R 1 9.5 602 10 035849 LECITHIN:CHOLESTEROL A 2 9.5 602 10 04364 CYCLOOXYGENASE 1. 2 602 10 04364 CYCLOOXYGENASE 1. 2 602 10 04364 CYCLOOXYGENASE 1SOFORM 2 9.4 83 2 049523 SORTILIN PRECURSOR. 4 9.3 154 2 015186 COLIAI AND PRGEB FUSIO 4	11.1 679 8 023352 HYPOTHETICAL 74.6 KD P 3 10.8 567 10 008770 PLATELET GLYCOPROTEIN 8 10.3 574 10 035298 ACYLOXYACL HYPOTHETICAL 74.6 KD P 3 154 10 035298 ACYLOXYACL HYPOTHES. 3 10.3 674 110 036463 PROLINE- AND LEUCINE-R 1 9.5 602 10 035849 LECTHHIN:CHOLESTEROL A 2 9.5 602 10 053844 CYCLOXYGENASE 15.9 5 602 10 063894 CYCLOXYGENASE 15.9 5 602 10 063894 CYCLOXYGENASE 15.9 9.3 154 2 015186 COLIAI AND POGFE FUSIO 4 9.3 154 2 015186 CCLIAI AND POGFE FUSIO 4 9.3 154 2 015354 C-SIS PROLO-ONCOGENE (4 4 4 6 1 5 015354 C-SIS PROLO-ONCOGENE (4 4 6 1 5 015354 C-SIS PROLO-ONCOGENE (4 5 0154554 C-SIS PROLO-ONCOGENE (4 5 015	11.1 679 8 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ALIGNMENTS

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ΔĪ	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
Œ	HYPOTHETICAL 74.6 KD PROTEIN.
SO	ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
Ö	EUKARYOTA; PLANTA; EMBRYOPHYTA; ANGIOSPERMAE; DICOTYLEDONEAE;
ဗ	CAPPARALES; CRUCIFERAE.
RN	[1]
85	SEQUENCE FROM N.A.
S	BEVAN M., SŢIEKEMA W., MURPHY G., WAMBUTT R., POHL T., TERRYN N.,
R.A	KREIS M., KAVANAGH T., ENTIAN K.D., RIEGER M., JAMES R.,
R.	PUIGDOMENECH P., HATZOPOULOS P., OBERMAIER B., DUESTERHOFT A., JONES J.,
S	PALME K., ANSORGE W., DELSENY M., BANCROFT I., MEWES H.W., SCHUELLER C.,
R.	CHALWATZIS N.;
H	SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN	[2]
RP	SEQUENCE FROM N.A.
Æ	EU ARABIDOPSIS SEQUENCING PROJECT, ESSA;
RL	SUBMITTED (JUN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
껆	EMBL; 297337; E326841;
KW	HYPOTHETICAL PROTEIN.
S.	SEQUENCE 679 AA; 74635 MW; B301B713 CRC32;
A Be	Query Match 11.1%; Score 106; DB 8; Length 679; Best Local Similarity 32.3%; Pred. No. 3.56e-02; Matches 20; Conservative 16; Mismatches 22; Indels 4; Gaps 4;
셤	598 KYCRSK-YETIHGONHDNAADVLELAIKREMPAELL-R-ASLRHTNEDORNFILLNVGRSA 654
ô	42 KTCSCRLYELLHGAG-NHAAGILTLGKRRPGPPGLQGRLQRLLQANGNHAAGILTMGRRA 100
	: : :: :

RESULT 2 PRELIMINARY; PRT; 567 AA.

1D 008770 AC 008770; PRELIMINARY; PRT; 567 AA.

1D 01-071L-1997 (TREMBIREL. 04, CREATED)

1D 01-071L-1997 (TREMBIREL. 04, LAST SEQUENCE UPDATE) 655 SP 656 :: 101 GA 102 g ò

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SORTILIN PRECURSOR
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ID Q99523
AC Q99523;
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                                                                                                                                                                                                                                    STRAIN-SPRAGUE-DAWLEY AND WISTAR; TISSUE-LIVER;
WANG J., ANDERSON R.A., PARKS J.S.;
SUBMITTED (JUL-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + STEROL = STERP +
1-ACYLGLYCEROPHOSPHOCHOLINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
02CCLOOXYGENNSE ISOFORM COX-1 (FRAGMENT).
RATTUS NORVEGICUS (RAT).
EUKARYOTA; MALAZOA; CHOKDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RATTUS NORVEGICUS (RAT).
EUKRRYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYCLOOXIGENASE 1.
RATIUS NORVEGICUS (RAI).
EUKARYOTA, METAZOA; CHORDAIA; VERTEBRAIA; TETRAPODA; MAMMALIA; EUTHERIA; RODENTIA.
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STRAIN=FISHER 344;

STRAIN=FISHER 344;

FENG L., SUN W., XIA Y., TANG W.W., CHANMUGAM P., SOYOOLA E.

WILSON C.B., HWANG D.;

WILSON C.B., HWANG D.;

ARCH. BICCHEM. BIOPHYS. 307:0-0(0).

EMBL; U03388; G415638; -.

SEQUENCE 602 AA; 69115 MW; DC2236E9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE; 94099619.
FENG L., SUN W., XIA Y., TANG W.W., CHANMUGAM P., SOYOOLA E.
WILSON C.B., HWANG D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 602;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 91; DB 10; Length 440
Pred. No. 2.56e+00;
2; Mismatches 5; Indels
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Pred. No. 2.56e+00;
7; Mismatches 15; Indels
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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WANG J., GEBRE A.K., ANDERSON R.A., PARKS J.S.; BIOCHIM. BIOPHYS. ACTA 1346:207-211(1997).
                                                                                                                                                                                                                                                                                                                                           EMBL; U62803; G2306762; -.
PROSITE; PS00120; LIPASE_SER; 1.
SEQUENCE 440 AA; 49882 NW; 6CC16087 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           602 AA
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063684,
063684,
01-NOV-1996 (TREMBLREL. 01, CR
01-NOV-1996 (TREMBLREL. 01, LA
01-NOV-1996 (TREMBLREL. 01, LA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Fuery Match 9.5%;
Best Local Similarity 62.5%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dery Match 9.5%;
Best Local Similarity 40.0%;
Matches 16; Conservative
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                         SEQUENCE FROM N.A
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EUKARYOTA, METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
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EUTHERIA; PRIMATES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
PETERSEN C.M., NIELSEN M.S., JACOBSEN L., TOMMERUP N., HOLM I ROIGAARD H., GLIEMANN J., MADSEN P., MOESTRUP S.K.;
SUBMITTED (FEB-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; X98248; E246784;
                                                                                                           Length 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                   7; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1997 (TREMBLREL. 03, CREATED)
01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                             1 MSRRSLSLQFPLLLLLLLPPPPVLLTDAGVPSPVIP-CC 39
                                                                                                                                                                                                                        69 LQRLLHGDPGEEDGAELDLNMTRSHSGGELESLA-RGRR 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |||||||:: |: :| :| || | ::|:|||: :|||| 79 LQRLLQAN-GNH-AAGI-LTMGR-RAGAELEPYPCPGRR 113
                                                                                                        Score 91; DB 10;
Pred. No. 2.56e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 9.3%; Score 89; DB 2; L
Best Local Similarity 43.6%; Pred. No. 4.40e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 90; DB 2; I
Pred. No. 3.36e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LT 10
015186
015186
015186
01-3186;
01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDAT
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDAT
COLLAL AND DECEB EUSION TRANSCRIPT (FRAGMENT).
HOMO SAPIENS (HUMAN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SORTILIN.
D2E351B9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154 AA; 16512 MW; 6DD0301B CRC32;
                                                                4 EBDC921 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Mismatches
ARCH. BIOCHEM. BIOPHYS. 307:361-368(1993).
EMBL; S67721; G460556; -.
                                                                                                                                                                                                                                                                                                                               833
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 WPHGLGLLLLLQLLPPSTLSQDRLDAPPPP 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                602 AA; 69158 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 33 P
34 833 S
833 AA; 92408 MW;
                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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Best Local Similarity 53.3%;
Matches 16; Conservative
                                                                                                        Query Match
Best Local Similarity 40.0%;
Matches 16; Conservative
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SUBMITTED (SEP-1997) TO
EMBL; Y08643; E293780;
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J. CELL BIOL. 124:949-961(1994).

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Score 88; DB 4; Length 1174;
Pred. No. 5.75e+00;
14; Mismatches 12; Indels
LEGUEDNCE FROM N.A.
MEDILINE; 96421547.
BEATCH M., PESAITIS L.A., GALLIN W., GOODENOUGH D.A.,
STEVENSON B.R.;
J. BIOL. CHEM. 271:25723-25726(1996).
                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
BEATCH M.;
BEATCH M.;
BEATCH Z.;
EMBL, 127152, 61536970; ...
SEQUENCE 1174 AA; 132085 MW; 2FA16883 CRC32;
                                                                                                                                                                           GOODENOUGH D.A.;
SUBMITTED (MAR-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
9.2%;
est Local Similarity 29.7%;
ttches 11; Conservative
                                                                                                                                              SEQUENCE FROM N.A.
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Search completed: Thu Jul 30 09:18:04 1998 Job time: 41 secs.

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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu Jul 30 09:16:51 1998; MasPar time 5.05 Seconds 646.000 Million cell updates/sec lar output not generated. : o o

>US-08-938-548A-6 (1-130) from US08938548A.pep 954 Description: Perfect Score: Sequence: Title:

1 MNLPSTKVPWAAVTLLLLLL......GRRCPTATATALAPRGGSRV 130

PAM 150 Gap 11 Scoring table:

69111 seqs, 25083644 residues

Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Statistics:

swiss-prot35 1:swiss1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 41.891; Variance 75.823; scale 0.552

SUMMARIES

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Pred. No.	1.78e-02	9.43e-02	9.43e-02	9.43e-02	9.43e-02	9.43e-02	2.50e-01	2.50e-01	4.74e-01	4.74e-01	4.74e-01	8.89e-01	8.89e-01	1.21e+00	1.21e+00	1.21e+00	1.65e+00	2.24e+00	2.24e+00	2.24e+00	2.24e+00	2.24e+00	2.24e+00
Description	SECRETIN PRECURSOR (FR	PHOSPHATIDYLCHOLINE-ST	FIBULIN-1, ISOFORM A P	FIBULIN-1, ISOFORM B P	FIBULIN-1, ISOFORM C P	FIBULIN-1, ISOFORM D P	FIBRIL-FORMING COLLAGE	ATRIAL NATRIURETIC PEP	COMPLEMENT C1Q SUBCOMP	PHOSPHATIDYLCHOLINE-ST	PHOSPHATIDYLCHOLINE-ST	PLATELET-DERIVED GROWT	SALIVARY PROLINE-RICH	INFECTED CELL PROTEIN	4-1BB LIGAND (4-1BBL).	SEC14 CYTOSOLIC FACTOR	PDGF-RELATED TRANSFORM	INFECTED CELL PROTEIN	HYPOTHETICAL PROTEIN H	FERRIC ENTEROBACTIN TR	PHOSPHATIDYLCHOLINE-ST	RETINAL GUANYLYL CYCLA	COMPLEMENT C3 PRECURSO
ΩI	SECR_PIG	LCAT_MOUSE	FBLA_HUMAN	FBLB_HUMAN	FBLC_HUMAN	FBLD_HUMAN	CAFF_RIFPA	ANPA_HUMAN	C1QB_HUMAN	LCAT_RAT	LCAT_HUMAN	PDGB_HUMAN	PRP1_HUMAN	ICP3_HSV1D	41BL_HUMAN	SC14_YARLI	TSIS_SMSAV	ICP3_HSV1N	YCEC_HAEIN	FEPD_ECOLI	LCAT_PAPAN	CYGD_HUMAN	CO3_RAT
8	Н	-	Н	-	-	-	П	-	Н	-	-	Н	Н	н	-	Н	Н	н	-	Н	н	Н	Н
Length	131	438	266	601	683	703	1027	1001	251	440	440	241	331	252	254	497	226	245	322	334	440	1103	1663
& Query Match	10.6	10.1	10.1	10.1	10.1	10.1	7.6	7.6	9.5	9.5	9.5	9.3	6.9	9.5	9.5	9.5	9.1	9.0	9.0	9.0	9.0	9.0	9.0
Score	101	96	96	96	96	96	93	66	91	91	91	89	83	88	88	88	87	86	98	98	98	98	98
Result		7	٣	4	5	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

3.03e+00	3.03e+00	3.03e+00	3.03e+00	4.09e+00	4.09e+00	4.09e+00	4.09e+00	4.09e+00	4.09e+00	4.09e+00	4.09e+00	5.50e+00	5.50e+00	5.50e+00	5.50e+00	5.50e+00	5.50e+00	5.50e+00	5.50e+00	5.50e+00	7.38e+00
PLACENTAL LACTOGEN I P	PLATELET-DERIVED GROWT	HYPOTHETICAL 28 KD PRO	LIPASE 1 PRECURSOR (EC	LYSIS PROTEIN.	E PROTEIN.	EPHRIN-A3 PRECURSOR (E	LIPASE 3 PRECURSOR (EC	HYPOTHETICAL 36.0 KD P	GIPASE ACTIVATING PROT	LUTROPIN-CHORIOGONADOT	PROTEIN-TYROSINE PHOSP	PLATELET GLYCOPROTEIN	OXALATE OXIDASE PRECUR	SL CYTOKINE PRECURSOR	PUTRESCINE TRANSPORT S	PHOSPHATIDYLCHOLINE-ST	HYPOTHETICAL 59.6 KD P	SERUM ALBUMIN PRECURSO	PROTEIN-TYROSINE PHOSP	ANGIOTENSIN-CONVERTING	GUANYLYL CYCLASE GC-E
PLC1_BOVIN	PDGB_MOUSE	YPE1_RHORU	LIP1_PSYIM	VGE_BPPHX	VGE_BPS13	EFA3_HUMAN	LIP3_MORSP	YCEC_ECOLI	RN_DROME	LSHR_PIG	PTPX_MOUSE	GPBB_PAPCY	OXO2_HORVU	FL3L_HUMAN	POTI_ECOLI	LCAT_RABIT	YABK_ECOLI	ALBU_CHICK	PTPX_RAT	ACE_RABIT	CYGE_MOUSE
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8.9	8.9	8.0	8.9	8.8	8.8	8.8	8.8	8.	8.8	æ æ	8.8	8.7	8.7	8.7	8.7	8.7	8.7	8.7	8.7	8.7	8.6
82	82	82	82	84	84	84	84	84	84	84	84	83	83	83	83	83	83	83	83	83	83
24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 ID SECK_PIG STANDARD; FRT; 131 AA. AC POL279; DT 21-JUL-1986 (REL. 01, CREATED) DT 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE) DT 01-APR-1990 (REL. 32, LAST ANNOTATION UPDATE) DE SECRETIN PRECURSOR (FRAGMENT). S SUS SCROFA (PIG), BOS TAURUS (BOVINE), AND CAVIA PORCELLUS (GUINEA OS PIG). C EUTRERIA: ARTIODACIYLA. R SEQUENCE FROM N.A. R SEQUENCE FROM N.A. R SEQUENCE FROM N.A. R SEQUENCE OF 30-56. R SECIES-PIG; RX MEDLINE; 70282334. R MEDLINE; 70282334. R MEDLINE; 70282334. R MEDLINE; 7028234. RA MUTT V. JORPEE J.E., MAGNUSSON S.; RL EUR. J. BIOCHEM. 15:513-519(1970). R SEQUENCE OF 30-59 AND 92-131. R SEQUENCE OF 30-59 AND 92-131.
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SPECIES-PIG; MEDLINE; 90370867. GAFVELIN G., JOERNVALL H., MUTT V.; PROC. NATL. ACAD. SCI. U.S.A. 87:6781-6785(1990). [4] SYNTHESIS OF 30-131.

SPECIES-FIG; BODANSZKY M., ONDETTI M.A., LEVINE S.D., NARAYANAN V.L., SALTZA M.V., SHEEHAN J.T., WILLIAMS N.J., SABO E.F.; CHEM. IND. 1757-1758(1966). [6]
SEQUENCE OF 30-56.
SPECIES-C.PORCELLUS;
MEDLINE; 90254163.
BUSCAIL L., CAUVIN A., GOURLET P., GOSSEN D., DE NEEF P., RATHE J., SEQUENCE OF 30-56.
SPECIES-BOVINE:
MEDLINE: 81237102.
CARLQUIST M., JOERNVALL H., MUTT V.;
FEBS LETT. 127:71-74(1981).

DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN

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RN [2]

RP SEQUENCE OF 30-44.

RA MEDIANES 9934537.

RA AGGRAVES W.S., DICKERSON K., BURGESS W.H., RUOSLAHTI E.;

RA AGGRAVES W.S., DICKERSON K., BURGESS W.H., RUOSLAHTI E.;

RL CELL 58:623-629(1989).

C. -: SIMCELLUARN COATION: EXTRACELLULAR MATRIX.

C. -: SIMCELLUARN COATION: EXTRACELLULAR MATRIX.

THERR C.TERMINAL REGIONS, ARE PRODUCED BY ALTERNATIVE SPLICING.

C. -: SIMILARITY: CONTAINS 3 ANAPHYLATOXIN-LIKE DOMAINS.

C. -: SIMILARITY: CONTAINS 3 ANAPHYLATOXIN-LIKE DOMAINS.

C. -: SIMILARITY: CONTAINS 3 ANAPHYLATOXIN-LIKE DOMAINS.

C. -: SIMILARITY: CONTAINS 9 EGF-LIKE DOMAINS.

C. -: SIMILARITY: CONTAINS 9 EGF-LIKE DOMAINS.

C. -: SIMILARITY: CONTAINS 9 EGF-LIKE DOMAINS.

C. -: SIMILARITY: STANDEST ST
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3 X ANNPHYLATOXIN REPEATS.
ANAPHYLATOXIN-LIKE 1.
ANAPHYLATOXIN-LIKE 2.
ANAPHYLATOXIN-LIKE 2.
ANAPHYLATOXIN-LIKE 3.
EGF-LIKE 2, CALCIUM-BINDING (EGF-LIKE 4, CALCIUM-BINDING (EGF-LIKE 5, CALCIUM-BINDING (EGF-LIKE 7, CALCIUM-BINDING (EGF-LIKE 7, CALCIUM-BINDING (EGF-LIKE 9, CALCIUM-BIN
     ARGRAVES W.S., TRAN H., BURGESS W.H., DICKERSON K.;
J. CELL BIOL. 111:3155-3164(1990).
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
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. No. 9.43e-02;
Mismatches 8;
BGF-LIKE 1

EGF-LIKE 2, CALCIUM-1

EGF-LIKE 3, CALCIUM-1

EGF-LIKE 6, CALCIUM-1

EGF-LIKE 6, CALCIUM-1

EGF-LIKE 7, CALCIUM-1

EGF-LIKE 9, CALCIUM-1

EGF-LIKE 9
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R -> SH (IN REF.
A2D23E14 CRC32;
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Pred. No.
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Best Local Similarity 57.1%;
Matches 16; Conservative
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MEDLINE; 93130909.

MEDLINE; 93130909.

MANN K., GALLL F., TIMPL R.;

EUR. J. BIOCHEM. 210:839-847(1992).

-!- SUBUNIT: HOMOTETRAMER.

-!- SUBUNIT: HOMOTETRAMER.

-!- PIM: ALL THE "X" ARE PROBABLY GLYCOSYLATED HYDROXYLYSINES.

PIR; S22915; 18BE.

BXTRACELLULAR MATRIX; CONNECTIVE TISSUE; REPEAT; HYDROXYLATION; GLYCOPROTEIN; COLLAGEN.

BY ANDROXYLATION; GLYCOROTEIN; COLLAGEN.

NONHELIAL REGION (N-TERMINAL).
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TRIPLE-HELICAL REGION.
NONHELICAL REGION (C-TERMINAL).
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                                                             01-JUL-1993 (REL. 26, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-JUL-1993 (REL. 26, LAST ANNOTATION UPDATE)
101-JUL-1-FORMING COLLAGEN ALPHA CHAIN.
RIFTIA PACHYPTILA (TUBE WORM).
EUKARYOTA, METAZOA; VESTIMENTIFERA.
                                 PRT; 1027 AA
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PROSITE; PS00012; EGE_1; FALSE_NEG.
PROSITE; PS01072; ANAPHYLATOXIN_1; 3.
PROSITE; PS01178; ANAPHYLATOXIN_2; 3.
PROSITE; PS01186; EGE_2; 3.
SIGNAL; ALTERNATIVE SPICING, 6.
SIGNAL; ALTERNATIVE SPICING, 6.
SIGNAL; ALTERNATIVE SPICING, 6.
REPEAT; PLASMA; EGF_LIGNE, CALCIUM-BINDING.
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1. No. 9.43e-02;
Mismatches 8; Indels
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3 X ANAPHYLATOXIN REPEATS.
ANAPHYLATOXIN-LIKE 1.
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EGF-LIKE 1.
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EGF-LIKE 6, CALCIUM-BINDING EGF-LIKE 6, CALCIUM-BINDING EGF-LIKE 7.
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Matches 16; Conservative
EMBL; U01244; G403533;
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HYDROXYLATION. HYDROXYLATION (PARTIAL). HYDROXYLATION.

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1-ACYLGLYCEROPHOSPHOCHOLINE (PALMITOYL, OLEOYL, AND LINOLEOYL CAN BE TARNSFERRED; A NUMBER OF STEROLS, INCLUDING CHOLESTEROL, CAN ACT AS ACCEPTOR).

ENZYME REGULATION: APOLIPOPROTEIN A-I IS A POTENT ACTIVATOR FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00120; LIPASE_SER; 1.
TRANSFERASE; ACYLTRANSFERASE; LIPID METABOLISM; GLYCOPROTEIN; SIGNAL.
1 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHOLESTEROL TRANSPORTED IN PLASMA LIPOPROTEINS.
-!- CAIALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + STEROL - STEROL ESTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SIMILARITY: PARTIAL WITH LIPASES (PANCREATIC, GASTRIC, HEPATIC,
LINGVAL, LIPOPROTEIN, BACTERIAL, ETC.).
EMBL; X54096; G56564; -.
PIR; S11214; XXRTN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1990 (REL. 16, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
01-NOV-1993 (REL. 26, LAST ANNOTATION UPDATE)
PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43)
(LECITHIN-CHOLESTEROL ACYLTRANSFERASE) (PHOSPHOLIPID-CHOLESTEROL ACYLTRANSFERASE))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LECITHIN-CHOLESTEROL ACYLTRANSFERASE. CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 4.74e-01;
6; Mismatches 1; Indels
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Q -> E (IN REF. 2).

N -> D (IN REF. 2).

G -> P (IN REF. 2 A).

1, 23D5197F CRC32;
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HYDROXYLATION.
GLUCOSYLGALACTOSE.
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GLUCOSYLGALACTOSE.
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                                                                                     HYDROXYLATION
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HYDROXYLATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity 53.3% Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 KIPWGSIPVLMLLLL 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |:||::::|:|||| 7 KVPWAAVTLLLLLLL 21
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P18424;
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ACT_SITE
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  MOD_RES
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PHILLOS. TRANS. R. SOC. LOND., B, BIOL. SCI. 306:345-354(1984).
-!- FUNCTION: C1Q ASSOCIATES WITH THE PROENZYMES C1R AND C1S TO YIELD C1, THE FIRST COMPONENT OF THE SERM COMPLEMENT SYSTEM. THE COLLAGEN-LIKE REGIONS OF C1Q INTERACT WITH THE CA(2+)-DEPENDENT C1R(2)C1S(2) PROENZYME COMPLEX, AND EFFICIENT ACTIVATION OF C1 TAKES PLACE ON INTERACTION OF THE GLOBULAR HEADS OF C1Q WITH THE FC REGIONS OF IGG NATIDEDY PRESENT IN IMMUNE COMPLEXES.
-!- SUBUNIT: C1 IS A CALCIUM DEPENDENT TRIMOLECULAR COMPLEXES.
R AND S IN THE MOLAR RATION OF 1:2:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- SUBUNIT: CLO SUBCOMPONENT IS COMPOSED OF NINE SUBUNITS, SIX OF WHICH ARE DISULFIDE-LINKED DIMERS OF THE A & B CHAINS, AND THREE OF WHICH ARE DISULFIDE-LINKED DIMERS OF THE C CHAIN.
-1- SIMILARITY: CONTAINS A CLQ DOMAIN.
EMBL; X03084; G573114; -
EMBL; X03084; G573114; -
EMBL; M36278; G179638; -
PIR; B23422; B23422.
MIM; 120570; -
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS01113; C1Q; 1. COMPLEMENT PATHWAY; PLASMA; HYDROXYLATION; GLYCOPROTEIN; COLLAGEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C10.
PYRROLIDONE CARBOXYLIC ACID.
INTERCHAIN (WITH CXS-26 IN CHAIN A).
                                                                                                                                                                                                                                                                                                                                                                   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                              ;
  Length 1061;
                                            10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPLEMENT C10, B CHAIN. COLLAGEN-LIKE.
                                                                                                                                                                                                                           P02746;
21-JUL-1996 (REL. 01, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
COMPLEMENT C1Q SUBCOMPONENT, B CHAIN PRECURSOR.
    Score 93; DB 1; I Pred. No. 2.50e-01;
                                          Mismatches
                                                                                                      251 AA
                                                                                  1 MPGPRRPAGSRIRLILLILLIPPLILLIRGSHAGNL 35
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BIOCHEM. J. 203:559-569(1982).
                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE; 86076906.
REID K.B.M.;
BIOCHEM. J. 231:729-735(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BIOCHEM. J. 179:367-371(1979)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 79041552.
REID K.B.M., THOMPSON E.O.P.;
BIOCHEM. J. 173:863-868(1978)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 224-251 FROM N.A.
  9.7%;
ilarity 48.6%;
Conservative
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MEDLINE; 82283890.
                                                                                                                                                                                                                                                                                                                                                    HOMO SAPIENS (HUMAN)
Query Match
Best Local Similarity
Matches 17; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 26-193.
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MEDLINE; 80020137.
REID K.B.M.;
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MEDLINE; 85038855.
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                                                                                                                                                                                                          C1QB_HUMAN
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DEPLIER C., D'ARCY A., WINKLER F.K., EGGIMANN B., HOSANG M.;
EMBO J. 11:3921-3926(1992).

-! FUNCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITOGEN FOR CELLS OF MESENCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO ITS AFFINITY RECEPPOR ELICITS A VARIETY OF CELLULAR RESPONSES. IT IS RELEASED BY PLATELETS UPON WOUNDING AND PLAYS AN IMPORTANT ROLE IN STIMULATING ADJACENT CELLS TO GROW AND THEREBY HEAL THE WOUND.
-! SUBGNIT: ANTIPARALLEL DISULFIDE-LINKED DIMER OF NONIDENTICAL (A AND B) CHAINS. HOMODIMER OF A AND B CHAINS ARE IMPLICATED IN TRANSFORMATION PROCESSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A-A AND B-B, AS WELL AS A-B, DIMERS CAN BIND TO THE PDGF RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDELINE; 83244981.
WATERFIELD M.D., SCRACE G.T., WHITTLE N., STROOBANT P., JOHNSSON A.,
WASTESON A., WESTERMARK B., HELDIN C.H., HUANG J.S., DEUEL T.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MUTAGENESIS, IMPORTANCE OF ARG-108 AND ILE-111 FOR RECEPTOR-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 92097530.
CLEMENTS J.M., BAWDEN L.J., BLOXIDGE R.E., CATLIN G., COOK A.L., CRAIG S., DRUMMOND A.H., EDWARDS R.M., FALLON A., GREEN D.R., HELLEWELL P.G., KIRWIN P.M., NAYEE P.D., RICHARDSON S.J., BROWN D., EMBO J. 10:4113-4120(1991).
                                           RAO C.D., IGARASHI H., CHIU I.-M., ROBBINS K.C., AARONSON S.A.;
PROC. NATL. ACAD. SCI. U.S.A. 83:2392-2396(1986).
                                                                                                                                                                                                                                                                                                                                           RATNER L., JOSEPHS S.F., JARRETT R., REITZ M.S., WONG-STAAL F.;
NUCLEIC ACIDS RES. 13:5007-5018(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                  RAO C.D., IGARASHI H., PECH M.W., ROBBINS K.C., AARONSON S.A.;
COLD SPRING HARB. SYMP. QUANT. BIOL. 51:959-966(1986).
                                                                                                                                     CHIU I.-M., REDDY E.P., GIVOL D., ROBBINS K.C., TRONICK S.R.,
                                                                                                                                                                                                                              MEDLINE; 85296313.
COLLINS I., GINSBURG D., BOSS J.M., ORKIN S.H., POBER J.S.;
NATURE 316:748-750(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BURGESS J., ODELL C.;
SUBMITTED (OCT-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 92283833.
ANDERSSON M., OSETWAN B., BAECKTROEM G., HELLMAN U.,
GERORGE-NASCIMENTO C., WESTERWARK B., HELDIN C.-H.;
J. BIOL. CHEM. 267:11260-11266(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WEICH H.A., SEBALD W., SCHAIRER H.U., HOPPE J.;
FEBS LETT. 198:344-348(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [13]
X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTONIADES H.N., HUNKAPILLER M.W.;
SCIENCE 220:963-965(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 26-241 FROM N.A. MEDLINE; 86164981.
                                                                                                  SEQUENCE OF 22-241 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NATURE 304:35-39(1983).
                                                                                                                                                      AARONSON S.A.;
CELL 37:123-129(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 82-110.
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         SEQUENCE FROM N.A. MEDLINE; 86205961.
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                                                                                                                                                                       PROSITE; PS00120; LIPASE_SER; 1.
TRANSFERASE; ACYLTRANSFERASE; LIPID METABOLISM; GLYCOPROTEIN; SIGNAL;
POLYMORPHISM; DISEASE MUTATION.
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LCAT DEFICIENCY).
FISH-EXE DISEASE).
LCAT DEFICIENCY; PARTIALLY
                                                                                                                                                                                                                                               LECITHIN-CHOLESTEROL ACYLTRANSFERASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
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21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
PLATELET-DERIVED GROWNH FACTOR, B CHAIN PRECURSOR (PDGF B-CHAIN)
(PDGF-2) (BACAPLERMIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE; 84250225.
JOSEPHS S.F., RATNER L., CLARKE M.F., WESTIN E.H., REITZ M.S.,
WONG-STAAL F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFICIENCY).
DEFICIENCY; LOSS
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N LCAT DEFICIENCY).
N FIGH-EYE DISEASE).
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N LCAT DEFICIENCY; LOS
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-> M (IN FISH-EXE DISEASE)
-> H (IN REF. 3).
69727CDF CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFICIENCY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 91; July,
Pred. No. 4.74e-01;
.......hes 3; Indels
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P -> L (IN FISH-EYF

G -> S (IN LCAT DEE

G -> R (IN LCAT DEE

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R -> W (IN LCAT DEE

R -> W (IN LCAT DEE

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M -> K (IN RISH-EYF

M -> I (IN RISH-EYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49578 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 81.3%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCIENCE 225:636-639(1984).
M26268; G187025; -. X04981; G34287; -. M17959; G386858; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 PWQWVTLLLGLLLPPA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 PWAAVTLILLILDPPA 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          345
371
257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        159
                                                            PIR, A00571, XXHUN.
PIR, A29661, A29661.
PIR, A25575, A25575.
PIR, 300036, 300036.
MIM, 136120, -..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            345
371
257
440 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     II 12
PDGB_HUMAN
P01127;
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VARIANT CONFLICT SEQUENCE

VARIANT

Query Match

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CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUR. J. IMMUNOL. 24:2219-2227(1994).
-!- FUNCTION: INDICES THE PROLIFERATION OF ACTIVATED PERIPHERAL BLOOD
T CELLS. MAY HAVE A ROLE IN ACTIVATION-INDICED CELL DEATH (AICD).
MAY PLAY A ROLE IN COGNATE INTERACTIONS BETWEEN T CELLS AND
121 HPPSRPFRLPPRLALRLRVTAEHLA-RLRL-RRAGGEGAPEPPATPATPATPATPAT 178
                            2; 94374434.
DN M.R., SMITH C.A., TOUGH T.W., DAVIS-SMITH T., ARMITAGE R.J., ROUX E., BAKER E., SUTHERLAND G.R., DIN W.S., GOODWIN R.G.; IMMUNOL. 24:2219-2227(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SUBGNIT: HOWOTRIMER (POTENTIAL).
-1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
-1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, PLACENTA, LUNG, SKELETAL MUSCLE AND KIDNEY.
-1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                       01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
4-1BB LIGAND (4-LBBL).
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00251; TNF 1; 1.
PROSITE; PS50049; TNF 2; 1.
CYTOKINE; TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL-ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 88; DB 1; Le
Pred. No. 1.21e+00;
4; Mismatches 1
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C68C1B27 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 9.2%;
Best Local Similarity 66.7%;
Matches 12; Conservative
                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                          :||
127 GSRV 130
                                                                                         179 PARV 182
                                                                                                                                                                                                                               41BL_HUMAN
P41273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE;
                                                                                                                                                                                                       RESULT
ID 41
AC P4
DT 01
DT 01
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:||| |: |||||:| 8 VPWAAVT-LLLLLLPPA 24

27 LPWALVAGLLLLLLLAAA 44

Search completed: Thu Jul 30 09:17:05 1998 Job time: 14 secs.

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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp : uo un:

Thu Jul 30 09:16:01 1998; MasPar time 7.56 Seconds 628.387 Million cell updates/sec

ular output not generated.

>US-08-938-548A-6 (1-130) from USO8938548A.pep 954 1 MNLPSIKVPWAAVTLLLLLL......GRRCPTATATALAPRGGSRV 130 Title:

Description: Perfect Score: Sequence:

Scoring table:

PAM 150 Gap 11

120441 seqs, 36531193 residues

Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Mean 39.951; Variance 87.022; scale 0.459 Statistics:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		dР					
Result	Score	Query	Query Match Length	DB	Ð	Description	Pred. No.
	101	10.6	131	-	SEPG	secretin precursor -	1.14e-01
7	100	10.5	495	~	JA0091	catalase (EC 1.11.1.6	1.52e-01
m	86	10.3	641	7	A45054	probable intercellula	2.72e-01
4	96	10.1	438	-	XXMSN	phosphatidylcholine	4.82e-01
2	96	10.1	601	~	B36346	fibulin 1 precursor,	4.82e-01
9	96	10.1	683	~	C36346	fibulin 1 precursor,	4.82e-01
7	93	9.7	1027	~	S28774	collagen alpha chain	1.12e+00
۵	. 93	9.7	1061		OYHUAR	natriuretic peptide r	1.12e+00
6	91	9.5	253	-	CIHUQB	complement subcompone	1.96e+00
10	91	9.5	440	-	XXRTN	phosphatidylcholine	1.96e+00
11	91	9.5	440	-1	XXHUN	phosphatidylcholine	1.96e+00
12	91	9.5	602	~	S39782	cyclooxygenase 1 - ra	1.96e+00
13	89	9.3	185	~	558383	hypothetical protein	3.38e+00
14	89	9.3	230	7	A55030	platelet-derived grow	3.38e+00
15	88	. 9.3	241	Н	PFHUG2	platelet-derived grow	3.38e+00
. 16	83	9.3	392	-	PIHUB6	salivary proline-rich	3.38e+00
17	89	9.3	602	~	S69198	prostaglandin G/H syn	3.38e+00
18	88	9.5	245	~	S43293		4.43e+00
19	88	9.5	491	~	JC6197	stromelysin 3 (EC 3.4	4.43e+00
20	88	9.5	497	~	S43745	phosphatidylinositol-	4.43e+00
21	87	9.1	226	Н	TVMVSS	PDGF-related transfor	5.79e+00
22	87	9.1	271	~	A25669	PDGF-related transfor	5.79e+00
23	. 87	9.1	583	~	I50518	DNA binding protein E	5.79e+00

7.56e+00 7.56e+00 7.56e+00 7.56e+00 7.56e+00 9.85e+00 9.85e+00 9.85e+00 9.85e+01 1.28e+01 1.28e+01 1.28e+01 1.28e+01	1.28e+01 1.28e+01
hypothetical protein ferric enterobactin t phosphatidylcholine- guanylate cyclase (Ec complement C3 precurs placental lactogen pr platelet-derived grow hypothetical protein triacylglycerol lipas triacylglycerol lipas gene E protein - phag gene E protein - phag protein log precursor triacylglycerol lipas triacylglycerol lipas lutropin-choriogonado lutropin-choriogonado lutropin-choriogonado lutropin-choriogonado lutropin-choriogonado NADH dehydrogenase (u GTPase-activating pro	Untropin-choriogonado Nypothetical protein
A35746 G64151 S16296 f G71509 HO01509 HO0170 C38T C38	, - 4
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40000000000000000000000000000000000000	444 445

ALIGNMENTS

			#formal_name Sus scrofa domestica #common_name domestic pig	on 12-Apr-1996 #text_change			M.B.; Leiter, A.B.	U.S.A. (1990) 87:2299-2303	recursor and tissue distribution					NID:g164670; PID:g164671		usson, S.	-519	n. The amino acid sequence.					ednenced	:		 	solation of a secretin precursor					1 GAF		Levine, S.D.; Narayanan,	J.T.; Williams, N.J.; Sabo, E.F.	the section of the second	ide amide with the normonar		synthesis confirmed the proposed structure of the natural	-	duodenal mucosa; duplication; hormone;	
	E	secretin precursor - pig	#formal_name Sus scrofa dome	24-Apr-1984 #sequence_revisi 20-Mar-1998	B35094; A01544; A36052			Proc. Natl. Acad. Sci. U.S.A	Secretin: structure of the p	#cross-references MUID:90192795	B35094	##molecule_type mRNA		s GB:M31496;	A91147	Mutt, V.; Jorpes, J.E.; Magnusson,	Eur. J. Biochem. (1970) 15:5	Structure of porcine secretin.	#cross-references MUID:70282334	A01544	_type		tryptic peptides were sequenced	A36052	Gatvelin, G.; Joernvall, H.; Mutt, V.	Proc. Natl. Acad. Sci. U.S.A	Processing of prosecretin: isolation of	irom porcine intestine.	#CIOSS-relerences MOID:903/080/	ASSOCIAL PARTY	two pretiminary	30-59.'R'.92-131 ##]abel	A90916	Bodanszky, M.; Ondetti, M.A.;	Saltza, M.V.; Sheehan, J.T	Chem. Ind. (1966) :1/5/-1/58 : Goodfeed of a boltonography amide with the bounces	synthesis of a neptacosapept activity of secretin.	annotation	synthesis confirmed the prop	normone *curorfamil: clucacon	٠.	
RESULT 1	ENTRY	TITLE	ORGANISM	DATE	ACCESSIONS	REFERENCE	#authors	#journal	#title	#cross-refere	#accession	##molecule	##residues	##cross-re	REFERENCE	#authors	#journal	#title	#cross-refere	#accession	##molecule	##residues	##note	REFERENCE	#authors	#journal	#title		#CIOSS-IEIEIE	*ACCR381011	##SCACUS ###0]66:10 +vpe		REFERENCE	#authors		#journal	#TITTE	#contents	#note	THE ACT HOLD A TO	KEYWORDS	1

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#submission
#description
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REFERENCE
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ENTRY
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                                                                                      Argraves, W.S.; Tran, H.; Burgess, W.H.; Dickerson, K.
J. Cell Biol. (1990) 111:3155-3164
Fibulin is an extracellular matrix and plasma glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #authors Argraves, W.S.; Tran, H.; Burgess, W.H.; Dickerson, K.
#journal J. Cell Biol. (1990) 111:3155-3164
#title Fibulin is an extracellular matrix and plasma glycoprotein
with repeated domain structure.
#cross-references MUID:91100426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #domain signal sequence #status predicted #label SIG\
#product fibulin 1 splice form C #status predicted
#label MAT\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Argraves, W.S.; Dickerson, K.; Burgess, W.H.; Ruoslahti, cell (1989) 58:623-629
Fibulin, a novel protein that interacts with the fibronec receptor beta-subunit cytoplasmic domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #binding_site carbohydrate (Asn) (covalent) #status
predicted
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
#formal_name Homo sapiens #common_name man
19-Apr-1991 #sequence_revision 19-Apr-1991 #text_change
29-Aug-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #formal_name Homo sapiens #common_name man
19-Apr-1991 #sequence_revision 19-Apr-1991 #text_change
10-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fibulin 1 precursor, splice form C - human fibulin C fibulin 1 splice form A; fibulin 1 splice form
                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                         Length 601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##molecule_type mRNA
##residues 1-566 ##label AR2
##cross-references GB:X53741; NID:931414; PID:931415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##residues 1-683 ##label ARG
##cross-references GB:X53743; NID:931418; PID:931419
                                                                                                                                                                                                                                                                                                                                                                                         Db 2,
. 4.82e-01;
. . 8;
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#map_position 22q13.3-22q13.3
KEYNORDS alternative splicing
#Hength 601 #molecular-weight 65485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##cross-references GDB:278285; OMIM:135820
#map_position 22q13.3-22q13.3
KEYWORDS alternative splicing; glycoprotein
                                                                                                                        #cross-references MUID:91100426
#accession B36346
                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                         Score 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #type complete
                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 VPLPLLLGGLALLAAGVDADVLLEACC 37
                                                                                                                                                                                                                     ##residues 1-601 ##label ARG
##cross-references GB:X53742
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#accession A32826
                                                                                                                                                                                                                                                                                                                                                                                     dery Match
Best Local Similarity 57.1%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                              GDB: FBLN1; FBLN
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##residues 1-601
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 ORGANISM
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[-95, x, 97-107, x', 109-191, x', 193-260, x', 262-278, x', 280-572, x', 574-611, x', 613-656, x', 658-737, x', 739-764, x', 766-809, x', 811-926, x', 928-935, x', 937-1027 ##label MAN we have shown the unidentified residues as Lys forming glycosylated 5-hydroxylysine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1-95,'X',97-107,'X',109-191,'X',193-260,'X',262-278,'X',
280-572,'X',574-611,'X',613-656,'X',658-737,'X',
73-764,'X',766-809,'X',811-926,'X',928-935,'X',
937-1027 ##label MAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       903-proline modified to 4-hydroxyproline was also found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##ccession $17581
##molecule_type protein
##molecule_type protein
##residues 8-45,525-545, X',547-566, X',568-572, X',574-611, X',
613-618; X',811-882 ##label GAI
MANENT Prolines and lysines at the third position of the tripeptide
repeating unit (G-X-Y) are hydroxylated to varying extents.
Prolines are predominately 4-hydroxylated in the Y-position and
both 3- and 4-hydroxylated in the X-position. Lysines are
5-hydroxylated and subsequently about 50% are O-glycosylated.
homotrimer
homotrimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #domain collagenous #status experimental #label COL\ #domain carboxyl-terminal telopeptide (fragment) #label
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                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #formal_name Riftia pachyptila
22-Nov-1993 #sequence_revision 09-Mar-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S22915
Mann, K.; Gaill, F.; Timpl, R.
submitted to the Protein Sequence Database, July 1992
Amino acid sequence and cell adhesion activity of a fibril-forming collagen from the tube worm Rifiia pachyptila living at deep sea hydrothermal vents.
S22915
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Engel, J.
#length 683 #molecular-weight 74475 #checksum 7443
                                                                                                                                                                                                                                                                                                                                                                                S28774 #type fragment collagen alpha chain - tube worm (Riftia pachyptila)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mann, R.; Gaill, F.; Timpl, R.
Bur. J. Blochem. (1992) 210:839-847
Amino-acid sequence and cell-adhesion activity of a
fibril-forming collagen from the tube worm Riftia
pachyptila living at deep sea hydrothermal vents.
$28774
                                                                                                                              ï
                                                             Length 683;
                                                                DB 2; L4
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                                                                                                                              3; Mismatches
                                                                Score 96;
Pred. No.
                                                                                                                                                                                                                               10 VPLPLLLGGLALLAAGVDADVLLEACC 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-May-1997
S28774; S22915; S17581
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#accession S17581
                                                                Query Match
Best Local Similarity 57.1%;
Matches 16; Conservative
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##residues 1-95,'X'
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##residues 1-95,'X'
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##molecule_type mRNA
##residues 1-44(
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                                                                                               Local Similarity
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KEYWORDS
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                                                                             Query Match
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                                 SUMMARY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##molecule_type protein
##residues
136-253 ##label RE4
##rose
116-Gix may also be present
The first component of complement is a calcium-dependent complex of
the three subcomponents Clq, Clr, and Cls. Subcomponent Clq binds
to immunoglobulin complexes, with resulting serial activation of
Clr (enzyme), Cls (proenzyme), and the other eight components of
complement.
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#product complement subcomponent Clq chain B #status
experimental #label MAT\
#domain collagenous, triple helix #label COL\
#domain complement Clq carboxyl-terminal homology #label
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CLASSIFICATION #superfamily complement subcomponent Clq chain A; complement Clq carboxyl-terminal homology Clq carboxyl-terminal homology complement pathway; glycoprotein; heterodimer; hydroxylysine; hydroxyproline; plasma; pyroglutamic acid; triple helix
                                                                                                                                                                                                                                                                                                                                                                                                                    residues
                                                                                                                                                          Reid, K.B.M.
Blochen. J. (1979) 179:367-371
Complete amino acid sequences of the three collagen-like
regions present in subcomponent clq of the first component
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reid, K.B.M.; Gagnon, J.; Frampton, J.
Biochem. J. (1982) 203:559-569
Completion of the amino acid sequences of the A and B chains
of subcomponent Clq of the first component of human
                                                                                                 as
                                                                                                                                                                                                                                                                                                                                                                        Reid, K.B.M.; Thompson, E.O.P.
Blochem. J. (1978) 173:863-868
Amino acid sequence of the N-terminal 108 amino acid residue
of the B chain of subcomponent Clq of the first component
of human complement.
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##molecule_type mRNA
##residues 28-753 ##label RE1
##cross-references EMBL:X03084
##note the codon ACA for residue 46
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experimental\
#binding_site carbohydrate (Lys) (covalent) #status
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                                                                                                                                                                                                                                                                                                          #cross-references MUID:79041552
#accession A90301
##molecule_type protein ##residues 28-99,'P',101-195 ##label RE3
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#accession B90315
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83,86,101,104,107
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28-253
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##residues 1-389,'G',391-440 ##label TAR ##residues 1-389,'G',391-440 ##label TAR ##cross-references EMBL:X54096; NID:956564
The active enzyme catalyzes the transfer of acyl groups from lecithin to sterol to form sterol esters. Palmitoyl, oleoyl, and linoleoyl residues can be transferred; a number of sterols, including cholesterol, can act as acceptor. Apolipoprotein A-I is a potent activator for this enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Meroni, G.; Malgaretti, N.; Magnaghi, P.; Taramelli, R.
Nucleic Acids Res. (1990) 18:5308
Nucleotide sequence of the cDNA for lecithin-cholesterol acyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #superfamily phosphatidylcholine--sterol acyltransferase
acyltransferase; glycoprotein; lipid metabolism; lipoprotein
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phosphatidylcholine--sterol O-acyltransferase (EC 2.3.1.43)
                                                                                                                                                                                                                                                                                                                                                                                    XXXTN #type complete phosphatidylcholine--sterol O-acyltransferase (EC 2.3.1.43)
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                                                                                                                                                                                                                                                                                                                                                                                                                                           precursor - rat
lecithin-cholesterol acyltransferase precursor;
phospholipid-cholesterol acyltransferase precursor
#formal_name Rattus norvegicus #common_name Norway rat
30.5ep-1993 #sequence_revision 30-Sep-1993 #text_change
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lecithin--cholesterol acyltransferase precursor;
phospholipid--cholesterol acyltransferase precursor
#formal_name Homo sapiens #common_name man
04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change
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experimental #1899 #checksum 7399
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                                                                                  Length 253;
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Pred. No. 1.96e+00;
                                                                                     Score 91; DB 1; L
Pred. No. 1.96e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transferase (LCAT) from the rat. #cross-references MUID:90384859
                                                                                                                                                  6; Mismatches
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                                                                                  9.5%;
Similarity 53.3%;
8; Conservative
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Best Local Similarity 62.5%;
Matches 15; Conservative
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S11214; S11302
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7 KVPWAAVTLLLLLL 21
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#authors Josephs, S.F.; Ratner, L.; Clarke, M.F.; Westin, E.H.; Reitz, M.S.; Wong-Staal, F.
#journal Science (1984) 225:636-639
#title Transforming potential of human c-sis nucleotide sequences encoding platelet-derived growth factor.
#cross-references MUID:84250225
#accession A94276
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Rao, C.D.; Igarashi, H.; Chiu, I.M.; Robbins, K.C.; Aaronson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #authors Antoniades, H.N.; Hunkapiller, M.W.
#journal Science (1983) 220:963-965
#title Human platelet-derived growth factor (PDGF): amino-terminal
amino acid sequence.
#cross-references MUID:83197379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chiu, I.M.; Reddy, E.P.; Givol, D.; Robbins, K.C.; Tronick, S.R.; Aaronson, S.A.
Cell (1984) 37:123-129
Nucleotide sequence analysis identifies the human c-sis proto-oncogene as a structural gene for platelet-derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #journal Proc. Natl. Acad. Sci. U.S.A. (1986) 83:2392-2396
#title Structure and sequence of the human c-sis/platelet-derived
growth factor 2 (SIS/PDGF2) transcriptional unit.
#accession A23532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Weich, H.A.; Sebald, W.; Schairer, H.U.; Hoppe, J.
FEBS Lett. (1986) 198:344-348
The human osteosarcoma cell line U-2 OS expresses a 3.8
kilobase mRNA which codes for the sequence of the PDGF-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##nolecule_type_nRNA
##residues 1-241 ##label RAO
##cross-references GB:M12783; GB:M16288; NID:g338210; PID:g338211
##Cross-references GB:M12783; GB:M16288; NID:g338210; PID:g338211
BNCE A93366
athors Collins, T.; Ginsburg, D.; Boss, J.M.; Orkin, S.H.; Pober,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature (1985) 316:748-750
Cultured human endothelial cells express platelet-derived
growth factor B chain: cDNA cloning and structural
   #formal_name Homo sapiens #common_name man
18.Apr-1984 #sequence_revision 20-Sep-1984 #text_change
                                                                                                 A94276; A21024; A23532; A93366; A25141; A94271; A93308;
A43499; S56115; I57635; I37266; A01380; A94622
A94276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##residues 1-241 ##label JOS
##cross-references GB:K01401; NID:g338206; PID:g338209
:NCE A21024
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##residues 1-241 ##label COL
##cross-references GB:X02811; NID:935371; PID:935372
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#cross-references MUID:85296313
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#accession A25141
                                                                       20-Mar-1998
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Deuel, T.F.; Huang, J.S.; Seeburg, P.H.; Gray, A.; Ullrich,
A.; Scrace, G.; Stroobant, P.; Waterfield, M.D.
EMBO J. (1994) 3:921-928
The c-sis gene encodes a precursor of the B chain of
platelet-derived growth factor.
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                                                                                                                                                                                S58383 #type complete
hypothetical protein 2 - human
#formal_name Homo sapiens #common_name man
12.Peb-1998 #sequence_revision 20-Feb-1998 #text_change
S58383
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Nucleic Acids Res. (1995) 23:2815-2822
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18.Nov-1994 #sequence_revision 18-Nov-1994 #text_change
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##cross-references EMBL:X83705
Y #holecular-weight 20774 #checksum 2728
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platelet-derived growth factor chain B precursor
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11; Mismatches 6; Indels
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##residues 1-18
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Thu Jul 30 09:18:22 1998; MasPar time 4.81 Seconds 158.235 Million cell updates/sec :uo

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>US-08-938-548A-6 (1-130) from USO8938548A.pep 954 1 MNLPSTKVPWAAVTLLLLLL......GRRCPTATATALAPRGGSRV 130 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

63816 segs, 5850866 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Mean 27.785; Variance 127.171; scale 0.218 a-issued 1:5_COMB 2:PCT9_COMB 3:backfiles Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	% Query Match Length DB	DB	A	Description	Pred. No.
	00		220		5175255-A	Datont NO 6176056	004039 8
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7	20	y.3	747	*	5194596-15	Patent No. 5194596.	7.65e+00
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4	8	9.3	241	~	PCT-US96-0	6	7.65e+00
'n	88	9.5	254	Н	US-08-236-	4	9.02e+00
٥	87	9.1	226	m	5498600-2		1.06e+01
7	87	9.1	241	٣	5175255-2	Patent No. 5175255.	1.06e+01
80	87	9.1	241	т	5175255-8	Patent No. 5175255.	1.06e+01
O	87	9.1	282	Н	US-08-445-	Sequence 1, Applicatio	1.06e+01
10	82	6.8	241	-	US-08-469-	13,	1.47e+01
11	82	8.9	613	~	PCT-US94-1	7	1.47e+01
12	84	8.8	238	н	US-08-240-	~	1.73e+01
13	84	8 8.	238	Н	US-08-453-	7	1.73e+01
14	84	8.8	1239	Н	US-08-026-	Sequence 3, Applicatio	1.73e+01
15	83	8.7	235	7	PCT-US94-0	ý	2.04e+01
16	83	8.7	235	Н	US-08-243-	ý	2.04e+01
17	82	8.6	241	ო	5219739-15	Patent No. 5219739.	2.39e+01
18	80	8.4	492	-	US-07-794-	Sequence 4, Applicatio	3.29e+01
19	80	8.4	492	Н	US-08-001-	4,	3.29e+01
50	80	8.4	1337	7	PCT-US95-0	Sequence 2, Applicatio	3.29e+01
21	79	8.3	589	~	PCT-US91-0	~	3.86e+01
22	79	8.3	589	Н	us-01-668-	7	3.86e+01
23	78	8.5	1184	Н	US-08-446-	Sequence 20, Applicati	4.52e+01

4 .52e+01 4 .52e+01 5 .52e+01 5 .52e+01 5 .30e+01 5 .30e+01 6 .19e+01 6 .19e+01 6 .19e+01 6 .19e+01 6 .19e+01 7 .24e+01 7 .24e+01			•		•		Gaps 5;					JOHN
Sequence 20, Applicati Sequence 8, Applicatio Sequence 8, Applicatio Sequence 5, Applicatio Sequence 5, Applicatio Sequence 10, Applicatio Sequence 10, Applicatio Sequence 36, Applicatio Sequence 2, Applicatio Sequence 52, Applicatio Sequence 52, Applicatio Sequence 52, Applicatio Sequence 52, Applicatio Sequence 52, Applicatio		AA.				;Nicholson, Margery FOR PURIFICATION OF PLATELET- /25,344	DB 3; Length 220; 4.65e+00; tches 6; Indels 5;	A-RGRR 60 : PCPGRR 113	1 AA.			M, JUDITH A.; FIDDES, SCULAR ENDOTHELIAL CE
US-08-446- US-08-097- US-08-097- US-08-073- US-08-483- US-08-284- US-08-284- US-08-284- US-08-283- US-08-283- US-08-283- US-08-283- US-08-283- US-08-283- US-08-283- US-08-283- US-08-031- US-08-469- US-08-469- US-08-469- US-08-469- US-08-469- US-08-485-	ALIGNMENTS	PRT; 238				en R DDS 3706 307	Score 92; Pred. No. 10; Misma	TRSHSGGELESLA :: : : : GR-RAGAELEPYP	PRI; 26			MUND G.; ABRA ODUCTION OF 2 TA: US/07/450,8
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APPLICANT: Thomason, Arlen R.;Nicholson, Margery
IIILE OF INVENTION: METHODS FOR PURIFICATION OF PLATELET-
DERIVED GROWTH FACTOR
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TITLE OF INVENTION: METHODS FOR PURIFICATION OF
DERIVED GROWTH FACTOR
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Pred. No. 1.06e+01;
11; Mismatches 6;
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 44 LQRLLQGDSGKEDGAELDLNMTRSHSGGELESLA-RGKR 81
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/25,344
FILING DATE: 23-MAR-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/25,344
FILING DATE: 23-MAR-1987
                                                                                                261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 241
ICE 261 AA; 29326 MW; 367179 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 241
SEQUENCE 261 AA; 29370 MW; 369384 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08445847A
                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 9.1%;
Local Similarity 43.6%;
nes 17; Conservative
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Local Similarity 43.6%;
les 17; Conservative
                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 9
                                                                                                STANDARD;
                                                                                                                                                                                                              Patent No. 5175255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 5175255
                                                                                                                                                                                                                                                   Patent No. 5175255
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                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO:2
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5175255-8
                                                                                            5175255-2
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Matches
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ID US:
XX AC XXX
XX XX DT
XX XX XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: MURRAY, MARK J.;KELLY, JAMES D.
TITLE OF INVENTION: BIOLOGICALLY ACTIVE MOSAIC PROTEINS
NUMBER OF SOUGHNES: 34
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/319,776
FILING DATE: 07-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 926,149
FILING DATE: 05-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 87; DB 3; Length 226;
Pred. No. 1.06e+01;
11; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
               OPERATING SYSTEM: Apple 7.5.3
SOFTWARE: Microsoft Word, Version #6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/236,918A
FILING DATE: 06-May-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 88; DB 1; L
Pred. No. 9.02e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29 LORLLOGDSGKEDGAELDLNMTRSHSGGELESLA-RGKR 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UDATA:
APPLICATION UNBER: US 08/060,843
FILING DATE: 07-May-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           245 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
FENCE 254 AA; 26624 MW; 316872 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 226
SEQUENCE 245 AA; 27563 MW; 324570 CN;
COMPUTER: Apple Power Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 379,239
FILING DATE: 11-JUL-1989
APPLICATION NUMBER: 941,970
FILING DATE: 15-DEC-1986
APPLICATION NUMBER: 896,485
FILING DATE: 3-AUG-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 705,175 FILING DATE: 25-FEB-1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 660,496
FILING DATE: 12-OCT-1984
                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 2
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                    TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID 00: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                     254 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 43.6%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 66.7%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 VPWAAVT-LLLLLLPPA 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 LPWALVAGLLLLLLLAAA 44
                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 5498600
                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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ID 5498600-2
XX
AC XXXXXX
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DT 01-JAN-1900
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CC Patent No.
CC Patent No.
CC APPLICA
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Indels

Length 241;

SEQUENCE

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282 AA

Length 241;

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Gaps

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Sequence 2, Application US/08453943
Patent No. 5738844
GENERAL INFORMATION:
APPLICANT: BECKMANN, M. P.
APPLICANT: CERRETI, DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE TITLE OF INVENTION: RECEPTOR HEK NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: GARLINGTON COUNTRY: USA COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: Apple MacIntosh OPERATING SYSTEM: Apple System 7.1 SOFTWARE: MICROSOFT WORD for Application DATA: APPLICATION DATA: 1995 FILING DATE: 30-MAY 1995 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 238;
                 Score 84; DB 1; Length 238;
Pred. No. 1.73e+01;
                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 84; DB 1; Len
Pred. No. 1.73e+01;
2; Mismatches 3;
                                                                                                                                                                               238 AA
                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/240,124
FILING DATE: 09-MAY-1994
APPLICATION NUMBER: US 08/161,132
FILING DATE: 03-DEC-199
FILING DATE: 03-DEC-199
FILING DATE: 03-DEC-199
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SEESE, KATHRYN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
HENCE 238 AA; 26350 MW; 315668 CN;
                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                          Sequence 2, Application US/08453943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 281
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                     Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 756822
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 238 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (206) 233-0644
                                                                                                                                                                               STANDARD;
                                                                                                 11 AAVILLILLIPP-ALLSL 28
                                                                                 2 AAAPLLILLLIVPVPLLPL 20
                 Query Match 8.8%;
Best Local Similarity 68.4%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 8.8%;
Best Local Similarity 68.4%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: SEATTLE STATE: WASHINGTON
                                                                                                                                                               JT 13
US-08-453-943-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX:
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Patent No. 551658
GENERAL INFORMATION:
APPLICANT: BECKMANN, M. P.
APPLICANT: CERRETI, DOUGLAS P.
AITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE TITLE OF INVENTION: RECEPTOR HEK
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: ALMINDEX CORPORATION
STREET: 51 UNIVERSITY STREET
                                                                                                                                                ö
                                                                                                            Score 85; DB 2; Length 613;
Pred. No. 1.47e+01;
13; Mismatches 18; Indels
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WEDIUM ITPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
OPERATING SYSTEM: Apple System 7.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,124
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                                                                                                                                                                                                                                                                          238
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 03-DEC-1993
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172,20
                                               TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
SEQUENCE 613 AA; 67034 MM; 1960405 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
FENCE 238 AA; 26350 MW; 315668 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 2814-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08240124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 238 amino acids
TYPE: amino acid
LENGTH: 613 AMINO ACIDS TYPE: AMINO ACID
                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                              Query Match 8.9%;
Best Local Similarity 31.1%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
                   TYPE: AMINO STRANDEDNESS:
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ID US-08-240-124-2
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SQ SEQUENCE 235 AA; 26415 MW; 293990 CN;

Score 83; DB 2; Length 235; Pred. No. 2.04e+01; 6; Mismatches 1; Indels Query Match
Best Local Similarity 55.6%;
Matches 10; Conservative

7 AWSPTTYLLLLLLSSGL 24 :1:: | ||||||||:::| 9 PWAAVT-LLLLLLLLPPAL 25

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Search completed: Thu Jul 30 09:18:32 1998 Job time : 10 secs.

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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu Jul 30 09:12:27 1998; MasPar time 5.42 Seconds 217.356 Million cell updates/sec .. 0

>US-08-938-548A-4 (1-28) from US08938548A.pep 196 not generated. hlar output Title:

1 RSGPPGLQGRLQRLLQASGNHAAGILTM 28 Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

140542 seqs, 42109429 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

sptrembl5
1:sp_fung1 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified Database:

Mean 29.922; Variance 51.029; scale 0.586 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

(SUMMARIES		
kesult		% Query					
No.	Score	Match	Match Length	DB	ID	Description	Pred. No.
-	76	38.8	1174	4	095168	TIGHT JUNCTION PROTEIN	1.91e-01
7	70	35.7	249	10	P97382	K+ CHANNEL BETA4 SUBUN	1.73e+00
٣	70	35.7	1277	10	035821	PAR INTERACTING PROTEI	1.73e+00
4	69	35.2	439	σ	052495	HRPE.	2.48e+00
ď	69	35.2	568	m	027212	ARTICULIN P60.	2.48e+00
9	69	35.2	1465	m	017909	н06001.2.	2.48e+00
7	99	34.7	178	σ	031955	YONC PROTEIN.	3.53e+00
ω	68	34.7	580	10	060811	RETINOID X RECEPTOR IN	3.53e+00
σ	29	34.2	462	ģ	P95644	RNA POLYMERASE SIGMA F	5.01e+00
10	67	34.2	510	თ	059913	RNA POLYMERASE SIGMA F	5.01e+00
11	49	34.2	514	σ	P77951	RNA POLYMERASE SIGMA F	5.01e+00
12	67	34.2	525	თ	059813	RNA POLYMERASE SIGMA F	5.01e+00
13	29	34.2	528	σ	059814	RNA POLYMERASE SIGMA F	5.01e+00
14	67	34.2	972	7	P89521	POLYPROTEIN.	5.01e+00
. 15	67	34.2	1841	σ	033958	TYLACTONE SYNTHASE MOD	5.01e+00
16	29	34.2	2115	~	014980	NUMA PROTEIN.	5.01e+00
17	67	34.2	2591	σ	054959	PRISTINAMYCIN I SYNTHA	5.01e+00
18	99	33.7	331	12	091640	LEUCINE ZIPPER WITH BA	7.09e+00
19	99	33.7	633	σ	007309	NODO.	7.09e+00
20	99	33.7	1344	10	035851	P160 MYB-BINDING PROTE	7.09e+00

21	65	33	~		062041	MOUSE 57-KD CALCIUM-BI	1.00e+01
22	65	33.	312	۵	033744		1.00e+01
23	9	33.	~		092931	3-HYDROXYISOBUTYRYL-CO	1.00e+01
24	65	33.	~		019452	F14D7.2.	1.00e+01
25	64	32.	_		031722	ORF263.	1.41e+01
56	64	32.	7		032855	METHYLTRANSFERASE.	1.41e+01
27	64	~	_		050983	CARA.	1.41e+01
28	64	\sim	_		027932	PROTEIN-TYROSINE PHOSP	1.41e+01
29	64	a	_		P76237	FROM BASES 1860594 TO	1.41e+01
30	64	32.	_		014976	HSGAK.	1.41e+01
31	63	N			050872	PUTATIVE SIGMA-54 DEPE	
32	63	~	1		P74570	HYPOTHETICAL 37.6 KD P	
33	63	~	_		091654	THYROID HORMONE INDUCE	
34	63	N			038350	ORF351.	1.97e+01
35	63	32.1	_		009636	HYPOTHETICAL 41.3 KD P	
36	63	N	_		082731	POLYPROTEIN.	
37	63	~	_		082720	POLYPROTEIN.	1.97e+01
38	62	ä			054084	HYPOTHETICAL 10.2 KD P	۲.
. 68	62	H			027642	DEOXYCYTIDINE-TRIPHOSP	2.75e+01
40	62	ä			005804	RNA-DIRECTED DNA POLYM	2.75e+01
41	62	31.6			026847	CONSERVED PROTEIN.	۲.
42	62	ä	ın		P79348	RETINA SPECIFIC RGS PR	۲.
43	62	H	5 476	~	013355	UNC-104 - AND KIF1A-REL	2.75e+01
44	62	4	6 574	σ	059532	RNA POLYMERASE SIGMA F	2.75e+01
45	62	ä	5 4	σ	007944	PRISTINAMYCIN I SYNTHA	۲.
					ALIGNMENTS		
RESULT 1	H 89		PRELIMINARY:	VARY	PRT:	1174 AA.	
AC 09516					Ì		

Gaps 20-2. CANIS FAMILIARIS (DOG). EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; CARNIVORA. Length 1174; SEQUENCE FROM N.A.
MEDLINE; 96421547.
BEALTH M., JESAITIS L.A., GALLIN W., GOODENOUGH D.A.,
STEVENSON B.R.;
J. BIOL. CHEM. 271:25723-25726(1996). BEATCH M.; SUBMITTED (AUG-1996) TO EMBL/GENBANK/DDBJ DATA BANKS. EMBL; LZ7152; G1536970; -SEQUENCE 1174 AA; 132085 MW; 2FA16B83 CRC32; GOODENOUGH D.A.; SUBMITIED (MAR-1994) TO EMBL/GENBANK/DDBJ DATA BANKS. LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE) CREATED) SEQUENCE FROM N.A.
MEDLINE; 94179414.
JESAITIS L.A., GOODENOUGH D.A.;
J. CELL BIOL. 124:949-961(1994) 02, 02, 05, Query Match 38.8%; Best Local Similarity 35.7%; Matches 10; Conservative 01-FEB-1997 (TREMBLREL. 01-FEB-1997 (TREMBLREL. 01-JAN-1998 (TREMBLREL. FIGHT JUNCTION PROTEIN [4] SEQUENCE FROM N.A. SEQUENCE FROM N.A.

ö 268 RSPSPELRGRPDHAGQPDSDRPIGVLLM 295 셤

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PRT; RESULT 2 ID P97382

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PRELIMINARY;

249 AA.

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
OGG
DD
OG
                Y K S
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RA AZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,
BORRISS R., BOURSIER L., BRANS A., BRAUN M., BRIGHELLS C., BRON S.,
RA BROULLET S., BRUSCHI C.V. CALDWELL B., CAPTER N.M.,
CHOI S.K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J., DANIEL R.A.,
BEQUILLET S., BRUSCHI C.V., CALDWELL B., CAPTER N.M.,
CHOI S.K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J., DANIEL R.A.,
BENTIAN K.D., ERRIGTON J., FABRET C., FERRARI E., FOULGER D., FRITZ C.,
GLASER P., GOFFEAU A., GOLIGHTLY E.J., GRANDI G., GUISEPI G., GUY B.J.,
GLASER P., GOFFEAU A., GOLIGHTLY E.J., GRANDI G., GUISEPI G., GUY B.J.,
HAGGA R., HAIECH J., HARWOOD C.R., HENNAT A., HILBERT H., HOLSAPPEL S.,
RASAHARA Y., KLAERR-BLANCHARD M., KURIN R., LAPIDUS A.,
KANDINGSTEIN G., KROGH S., KUMANO M., KURITA K., LAPIDUS A.,
LANDINOIS S., LAUBER J., LAZARRYLU V., KDELLAD R.P., MIZUNO M.,
RANDINGSTEIN G., RROGH S., NOBACK M., NOONE D., O'REILLY M., CORTEELLE D.,
RASHIN B.S., WAUEL C., MEDIGUE C., MEDINA N., REILADO R.P., PURNELLE B.,
ROCHWARA A., OUDEGA B., PARK S.H., PARKO V., POHL T.M., PORTETELLE D.,
RACHREE B., ROSE M., SADALE Y., SEKIGUCHI J., SEKOWSKA A., SEROR S.J.,
SERNOR P., SHIN B.S., SOLDO B., SOROKIN B., TAKARASHI H., TAKARARU K., TAKEUCHI M., TAMANGSHI T.,
TAKAHASHI H., TAKEWARU K., TAKEUCHI M., TAMANGSHI T.,
TAKAHASHI H., TAKEWARU K., VIARI A., VANDENBOL M.,
TAKAHASHI H., TAKEWARU K., VANDENBOL M.,
TAKAHASHI H., TAKEWARU K., VANDENBOL M.,
TAKAHASHI H., TAKEWARU K., YANDENG H., YANDENBOL M.,
TAKAHASHI H., TAKEWARU K., YORU YANDENBOL M.,
TAKAHASHI H., TAKEWARU K., YORU YANDENBOL M.,
TAKAHASHI H., TAKEWARU K., YORU YAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                    SEQUENCE FROM N.A.

WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,

BONTIELD J., BUTTON J., CONFEIT J., COOPER J., COULSON A.,

CRATTON M., DEAR S., DU Z., DURBIN R., FOWELLO A., FULTON L.,

GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,

JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,

LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,

PARSONS J., PERCY C., RIFREN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,

SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,

THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,

WATURE 368:32-38(0).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BACILLUS SUBTILIS.
PROKARYOTA: FIRMICUTES; ENDOSPORE-FORMING RODS AND COCCI; BACILLACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 69; DB 3; Length 1465;
Pred. No. 2.48e+00;
3; Mismatches 1; Indels
SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL: 292970; E349623; -.
PROSITE; PS00598; CHROMO_1; 2.
SEQUENCE 1465 AA; 169391 MW; F959D52F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1998 (TREMBLREL. 05, 01-JAN-1998 (TREMBLREL. 05, 01-JAN-1998 (TREMBLREL. 05,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 35.2%;
Local Similarity 69.2%;
les 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NATURE 390:249-256(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               700 QGRLQQLLKSSGK 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                031955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tches
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        REPRESENTATION OF THE STATE OF 
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BARRIL A., CONCRA M.I., FIGUEROA J., LEON G.;
SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
-- FUNCTION: THE SIGMA FACTOR IS AN INTITATION FACTOR THAT PROMOTES
ATTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Y10835; E294130; -.
PROSITE; PS00715; SIGMA70_1; 1.
PROSITE; PS00716; SIGMA70_2; 1.
TRANSCRIPTION REGULATION; SIGMA FACTOR; DNA-DIRECTED RNA POLYMERASE;
                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 67; DB 9; Length 462;
Pred. No. 5.01e+00;
11; Mismatches 4; Indels
                                                                   Score 68; DB 9; Length 1/8; Pred. No. 3.53e+00; ....ma+rhes 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
RETINGID X RECEPTOR INTERACTING PROTEIN 110 (FRAGMENT).
  TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EUBACTERIA; FIRMICUTES; ACTINOMYCETES; RENIBACTERIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-WAY-1997 (TREMBLREL. 03, CREATED)
01-WAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 68; DB 10; Ler
Pred. No. 3.53e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     462 AA; 50504 MW; E54BBFE5 CRC32;
SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATP
EMBL; 299115; E1183561; -.
SEQUENCE 178 AA; 19609 WW; CA7B8EDO CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                580 AA; 64852 MW; 28DA7406 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              462 AA
                                                                                                                                                                                                                                                                                                               580 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 95280959.
SEOL W., CHOI B.S., MOORE D.D.;
MOL. ENDOCRINOL. 9:72-85(1995).
EMBL; UZ2015; G709961; -.
MGD; MGI:103185; RXRIP110.
                                                                                                                                                                            70
                                                                                                                                                                                                                    7 LOGRIORLIQASGNHAAGIL 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.2%;
llarity 31.8%;
Conservative
                                                                                                                                                                                                                                                                                    17 8 9 060811 060811; 01-1007-1996 (TREMBLREL 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               485 QGRLLSLLEQSEHRTTGV 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNA POLYMERASE SIGMA FACTOR
                                                                                      Query Match 34.7%;
Best Local Similarity 45.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 44.4%; tes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||||| ||: | ::::|:
QGRLQRLLQASGNHAAGI 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RENIBACTERIUM SALMONINARUM
                                                                                                                                                                            1 MATRLQKALTEVGNHTTGNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THEN IS RELEASED
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                                                                                                                                                                                                                                                                                                                                                                                                                                            RXRIP110 OR RIP110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EUTHERIA; RODENTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-LIVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA-BINDING
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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ID P95644
AC P95644;
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STREPTOMYCES FRADIAE.
PROKARYOTA: FIRMICUTES; ACTINOMYCETALES; STREPTOMYCETACEAE.
                                                                                                                                                                                                                                                                                                                              Score 67; DB 11; Length 972;
Pred. No. 5.01e+00;
10; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 67; DB 9; Length 1841;
Pred. No. 5.01e+00;
9; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEHOFF B.S., SUTTON K.L., ROSTECK P.R. JR.;
SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U78289; G2317864; -.
PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.
                                                                                                                                                                                                               SUZUKI S., KIMURA M., KUSUDA R.;
SUBMITIED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AD006783; D1019990; -.
EMBL; AD006783; D1022914; -.
                                                                                                                                SUZUKI S., KIMURA M., KUSUDA R.;
SUBMITTED (MAR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                VIRUSES; DSRNA VIRUSES; BIRNAVIRIDAE; BIRNAVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1841 AA; 191190 MW; 2FF1A058 CRC32;
                                                                                                                                                                                                                                                                                                972 AA; 106767 MW; 9905CAOD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1841 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN'1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQ
01-JAN-1998 (TREMBLREL. 05, LAST ANN
                                                                                                                                                                                                                                                                                                                                                                                              731 RTTASGMDEELQKLLHATMARAKEV 755
                                                                                                                                                                                                                                                                                                                                                                                                                  1 RSGPPGLQGRLQRLLQASGNHAAGI 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYLACTONE SYNTHASE MODULE 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                            74.2%;
Local Similarity 32.0%;
nes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jery Match 34.2%;
sst Local Similarity 33.3%;
stches 8; Conservative
                                                                                                SEQUENCE FROM N.A. STRAIN-Y-6;
                                                                                                                                                                             SEQUENCE FROM N.A.
                                                SP.
                                                                                                                                                                                                                                                                               OLYPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSFERASE
SEQUENCE
                                                                                                                                                                                                 STRAIN-Y-6;
                                                BIRNAVIRUS
                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                ery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JT 15
033958
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                                                                                                                                                                                                                                                                                                                                                                Matches
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Search completed: Thu Jul 30 09:12:50 1998 Job time: 23 secs. ò

1513 RDTPAALAAHLAELLATARDHGPG 1536

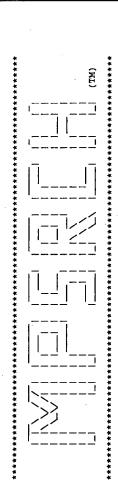
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Matches

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Gaps

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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu Jul 30 09:14:41 1998; MasPar time 5.30 Seconds 376.024 Million cell updates/sec Sular output not generated. : 0

>US-08-938-548A-6 (1-130) from US08938548A.pep 954

1 MNLPSTKVPWAAVTLLLLLL......GRRCPTATATALAPRGGSRV 130 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

124785 seqs, 15338987 residues Searched:

Minimum Match 0% Listing first 45 summarles Post-processing:

Database:

a-geneseg31-2
l:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27

Mean 29.913; Variance 129.900; scale 0.230 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query Match	l Query Match Length DB	DB	ID	Description	Pred. No.
П	96	10.1	566	5	R11148	Fibulin A.	5.91e+00
7	96	10.1	601	~	R11149	Fibulin B.	5.91e+00
m	96	10.1	683	7	R11150	Fibulin C.	5.91e+00
4	91	9.5	440	N	P70134	Natural recombinant h	1.39e+01
'n	91	9.5	440	25	W24789	Human lecithin-choles	1.39e+01
9	89	9.3	190	σ	R50012	Truncated Platelet de	1.94e+01
7	83	9.3	216	12	R68617	Human PDGF-B precurso	1.94e+01
&	83	9.3	220	œ	R40965	rPDGF B.	1.94e+01
σ	83	9.3	241	σ	R50009	Platelet-derived Grow	1.94e+01
10	83	9.3	241	12	R63469	Recombinant platelet	1.94e+01
11	88	9.3	241	σ	R50002	Platelet-derived Grow	1.94e+01
12	83	9.3	241	ω	R40964	PDGF Bc-sis.	1.94e+01
13	83	9.3	241	Н	P80596	Recombinant platelet	1.94e+01
14	88	9.5	252	4	R21708	HSV-1 (CVG-2) ICP34.5	2.30e+01
12	88	9.5	254	12	R64190	Human 4-1BB-L polypep	2.30e+01
16	88	9.2	254	25	W26657	Human 4-1BB ligand.	2.30e+01
17	87	9.1	111	7	R35515	Tryptophan aporepress	2.72e+01
18	87	9.1	190	12	R60615	Human PDGF-B 109 subu	2.72e+01
19	87	9.1	201	4	R21443	Sequence encoded by p	2.72e+01

2.72ee+01 2.72ee+01 2.72ee+01 2.72ee+01 2.72ee+01 3.72ee+01 3.73ee+01 3.73ee+01 3.74ee+01
v-sis protein p28sis. Cv-sis gene encoded P Recombinant platelet CV-sis gene product. Recombinant platelet Recombinant platelet Funan PDGF B19 link Funan PDGF B 19 link Funance encoded by t Sequence encoded by t Sequence encoded by t Sequence encoded by t Sequence encoded by t Funance encoded by t Funan endothelin bomb Truncated E protein f Eph transmembrane tyr Human hek-L protein f Eph transmembrane tyr Human Ref-L protein. Glutamic acid recepto Human S86/S109 Flt3 I Human Flt-3 ligand. S. clavuligerus ORF1 Amino acid sequence o Human Platelet Derive WIld-type avidin prot WZY (Rfc) protein inv
R22673 P80597 R4609672 R4609672 P80595 P80595 P80595 R63468 R61690 P81029 P8102
117 117 117 117 117 117 117 117 117 117
222 2411 2411 2411 2711 2711 2711 2711 2
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0110845000000000000000000000000000000000

ALIGNMENTS

					fibronectin.				ě				glycosylation		glycosylation	glycosylation		-					region						capeptide			pentapeptide				pentapeptide			
	Protein; 566 AA.		st entry)		adhesion; receptor;		Location/Qualifiers	. 29	/label= signal sequence		/label= fibulin A	æ	bel- N-linked		/label- N-linked glyc 339	N-linked		/label= type I motif	/label= repeat unit l	7	/label = repeat unit 2	$\boldsymbol{\sigma}$	/label= Glu/Asp-rich region		/label= type II motif	:	/label= repeat unit 1	15219	/label= consensus pentapeptide	47	/iabel= repeat unit 2 261265	consensus	10	label - repeat unit 3		/label= consensus pen	12334 abol	label= repeat unit 4 55 359	:
ILT 1	R11148 standard; Protein;	R11148;	21-MAY-1991 (first		rin;			tide		protein 3		modified_site 98	·	modified_site 5	modified site 3		region 3			region		region		region 1		region 1		region 2		region	region 2		region 2	•	region 3	•	region	region	n
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Thu Jul 30 09:11:23 1998; MasPar time 4.07 Seconds 251.156 Million cell updates/sec ular output not generated. Run on:

>US-08-938-548A-4 (1-28) from USO8938548A.pep 196 1 RSGPPGLOGRLOALOASGNHAAGILIM 28

Title: Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

120441 seqs, 36531193 residues Searched:

Post-processing: Minimum Match, 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 30.060; Variance 54.689; scale 0.550

SUMMARIES

Pred. No.	3.92e+00	3.92e+00	5.47e+00	7.60e+00	7.60e+00	7.60e+00	7.60e+00	7.60e+00	7.60e+00	7.60e+00	1.05e+01	1.45e + 01	1.45e+01	2.00e+01	2.00e+01	2.00e+01	2.00e+01	2.00e+01	2.00e+01	2.00e+01	2.00e+01	2.74e+01	2.74e+01
Description	hrpE protein - Pseudo	mALDP protein - mouse	hypothetical protein	-	transcription initiat	transcription initiat	transcription initiat	transcription initiat	YOR1 protein - yeast	٠	E2 protein - human pa	calcium-binding prote	adenylate cyclase (EC	hypothetical protein	BGRF1 protein - human	ribosomal protein S2,	hypothetical protein	protein-tyrosine-phos	protein-tyrosine-phos	hypothetical protein		pulmonary surfactant	pulmonary surfactant
А	S61858	S47044	E69913	JH0496	S11712	S41307	JN0443	JN0445	S64616	S23647	S36593	S26481	A33988	S51155	QQBE38	A42115	S76929	A46101	B46101	B64939	H64888	LNHUPS	LNHUP1
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Length DB	439	736	178	442	442	510	525	528	1477	2115	461	178	1692	263	325	394	400	535	548	556	879	248	248
% Ouery Match	35.2	35.2	34.7	34.2	34.2	34.2	34.2	34.2	34.2	34.2	33.7	33.2	33.2	32.7	32.7	32.7	32.7	32.7	32.7	32.7	32.7	32.1	32.1
Score	69	69	. 68	67	67	49	67	67	29	67	99	65	65	64	64	64	64	64	64	64	9	63	63
Result No.		~	9	4	S	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23

2.74e+01 2.74e+01 2.74e+01	2.74e+01 2.74e+01 2.74e+01 2.74e+01	2.74e+01 3.75e+01 3.75e+01 3.75e+01 3.75e+01	3.75e+01 3.75e+01 3.75e+01 3.75e+01	3.75e+01 3.75e+01 3.75e+01 3.75e+01 3.75e+01
pulmonary surfactant pulmonary surfactant- hypothetical protein	annexin iii Tat hypothetical protein hypothetical protein ecdysone receptor - f genome polyprotein -	PASI protein - yeast allergen TBA-1 - Toxo transcription factor hypothetical protein hypothetical protein	RNA-directed DNA poly conserved hypothetica carboxypeptidase (EC sulfite reductase (fe	genome polyprotein . itrite reductase (NA fatty-acid synthase (fatty-acid synthase (fatty-acid synthase (
LNHUP6 IS1921 Q3YCRQ	576765 509852 A41055 GNXSIV	A55152 B49139 S48361 S49183 B64899	S19248 F69200 JC2294 RDYCS7	GNXSN1 A49848 A57788 B57788 G01880
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ALIGNMENTS

<pre>S61858</pre>	SG1858 SG1846 van Gijsegem, F.; Gough, C.; Zischek, C.; Niqueux, E.; Arlat, M.; Genin, S.; Barberis, P.; German, S.; Castello, P.;	Mol. Microbiol. (1995) 15:1095-1114 The hrp gene locus of Pseudomonas solanacearum, which controls the production of a type III secretion system, encodes eight proteins related to components of the bacterial flagellar blogenesis complex.	s6 _ty fer	hrpE 4 #superfamily H+-transporting ATP synthase alpha chain homology	#domain H+-transporting ATP synthase alpha chain homology #label ATP #length 439 #molecular-weight 47533 #checksum 9718	1 35.2%; Score 69; DB 2; Length 439; Similarity 44.4%; Pred. No. 3.92e+00; 12; Conservative 7; Mismatches 8; Indels 0; Gaps 0;	281 RGFPPSVFAELPRLLERAGMSAAGSIT 307 : ::: :: : 1 RSGPPGLQGRLQRLLQASGNHAAGILT 27	S4704 #type complete mALDP protein - mouse #formal_name Mus musculus #common_name house mouse 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 847044
KESULI ENTRY TITLE ORGANISM DATE	ACCESSIONS REFERENCE #authors	#journal #title	#accession ##status ##molecule ##residues ##cross-re	GENETICS #gene CLASSIFICATION	FEATURE 191-359 SUMMARY	Query Match Best Local S Matches	Db 281 RGFP 1: Qy 1 RSGP	RESULT 2 ENTRY TITLE ORGANISM DATE ACCESSIONS

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##molecule_type DNA
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Four genes in Streptomyces aureofaciens containing a domain characterstic of principal sigma factors.
                                                                 *superfamily transcription initiation factor sigma katF; transcription initiation factor sigma katF homology
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transcription initiation factor sigma homolog hrdB -
Streptomyces aureofaciens
#formal_name Streptomyces aureofaciens
30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
08-Sep-1997
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homology #label KTF
#length 510 #molecular-weight 55795 #checksum 1415
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Pred. No. 7.60e+00;
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Pred. No. 7.60e+00;
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EMBL: X52983; NID: 948744; PID: 948745
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                 ##experimental_source strain A3(2)
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Similarity 31.8%;
7; Conservative
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Matches 7; Conservative
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Gene (1992) 12:68-70
Four genes in Streptomyces aureofaciens containing a domain
characterstic of principal sigma factors.
                                                                                                              *superfamily transcription initiation factor sigma katF; transcription initiation factor sigma katF homology DNA binding; sigma factor; transcription initiation
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transcription initiation factor sigma katf homology
DNA binding; sigma factor; transcription initiation
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streptomyces aureofaciens
#formal_name Streptomyces aureofaciens
30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
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homology #label KTF
#length 528 #molecular-weight 57598 #checksum 7360
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#length 525 #molecular-weight 57204 #checksum 9676
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YOR1 protein - yeast (Saccharomyces cerevisiae)
protein 69537; protein YGR281w
#formal_name Saccharomyces cerevisiae
17-May-1996 #sequence_revision 17-May-1996 #tex*
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Pred. No. 7.60e+00;
....matches 5; Indels
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##cross-references GB:M90412; NID:g153308; PID:g153309
##residues 1-525 ##label KOR
##cross-references GB:M90411; NID:g153305; PID:g153306
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Pred. No. 7.60e+00;
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Best Local Similarity 36.4%;
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Best Local Similarity 31.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Conservative
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Search completed: Thu Jul 30 09:11:43 1998 Job time: 20 secs.
                                           ##residues
                                                                                                                                                                                                                                                                 CLASSIFICATION
SUMMARY
                                                                                                                                                                #journal
#title
                                                                                                   #authors
                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                  å
                                                                                                                                                                                                     #superfamily leucine-rich alpha-2-glycoprotein repeat
homology; yeast adenylate cyclase catalytic domain homology
phosphorus-oxygen lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Landgren, M.; Zetterstrand, M.; Sundberg, E.; Glimelius, K. submitted to the EMBL Data Library, January 1995 Mitochondrial analysis revealed transcription of an ORF 3 of the atp6-gene and translation of a 32 kD protein in allophasmic male sterile Brassica lines containing the B. tournefortil cytoplasm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #authors Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, B.G.
#journal Mol. Biol. Med. (1983) 1:21-45
#title Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8
#cross-references MUID:85035713
                                                                                                                    ##residues______1-1692 ##label YAM
##cross-references GB:MA4942; NID:9173378; PID:9173379
##note the authors translated the codon TGC for residue 626 as
Ser, and GCC for residue 1243 as Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QQBE38  #type complete
BGRI protein - human herpesvirus 4 (strain B95-8)
#formal_name human herpesvirus 4, Epstein-Barr virus
25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #formal_name mitochondrion Brassica tournefortii
19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change
10-Sep-1997
S51155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                         homology #label YACC
#length 1692 #molecular-weight 190332 #checksum 2609
                                                                                                                                                                                                                                                                                      #domain yeast adenylate cyclase catalytic domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mitochondrion
mitochondrion
#length 263 #molecular-weight 29082 #checksum 9529
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hypothetical protein 263 - Brassica tournefortii
mitochondrion
                                                                                                                                                                                                                                                                                                                                                                   Length 1692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##residues 1-263 ##label LAN
##cross-references EMBL:X83692; NID:g633155; PID:g633157
                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 64; DB 2; Length 263;
Pred. No. 2.00e+01;
4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                   Score 65; DB 2; Lv
Pred. No. 1.45e+01;
                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A43044; A03782; S33034
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7 LQGRLQRLLQASGNHAAGIL 26
                                                                               preliminary
                                                                                                                                                                                                                                                                                                                                                                 33.2%;
llarity 57.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 32.7%;
Best Local Similarity 45.0%;
Matches 9; Conservative
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##residues 1-26
                                                                                                     ##molecule_type DNA
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Best Local Similarity
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#description
                                                                                                                                                                                                       CLASSIFICATION
                                                                                 ##status
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                                                              #accession
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1328-1413
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#authors
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ORGANISM
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Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.;
Farrell, P.J.; Gibson, T.J.; Hatfull, G.; Hudson, G.S.;
Satchwell, S.C.; Seguin, C.; Tuffnell, P.S.; Barrell, B.G.
Nature (1984) 310:207-21
DNA sequence and expression of the B95-8 Epstein-Barr virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                              #cross-references MUD:84270667
#contents annotation; protein coding region
SSIFICATION #superfamily herpesvirus 38K protein
#ength 325 #molecular-weight 36462 #checksum 3547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                            ##cross-references EMBL:V01555; NID:g59074; PID:g1334893
NCE A03794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 64; DB 1; Length 325;
Pred. No. 2.00e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches 10; Indels
##molecule_type DNA
##residues 1-325 ##label BAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 PELRDTLQRLLPPPNLEDSEALT 126
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Best Local Similarity 39.1%;
Matches 9; Conservative
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CARBOHYD

CARBOHYD CARBOHYD SEQUENCE

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RESULT

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-!- IN CONTRAST TO TEAST OFFICE CYCLASE S. POMBE CYCLASE IS NOT LIKELY TO B REGULATED BY RAS PROTEINS.
-!- SIMILARIY: THE REPEATED LEUCINE-RICH (LRR) SEGMENT IS FOUND IN MANY PROTEINS. NUMBER IN THIS PROTEIN: 22.
-!- SIMILARIY: BELONGS TO CLASS-3 OF ADENYIKL CYCLASES.
-!- SIMILARIY: CONTAINS A PP2C-LIKE DOMAIN.
EMBL; M26492; G173379; --
PEMBL; M34942; G173379; --
PEMBL; A33988; A33988.
PIR; A33539; A33539.
YAMAWAKI-KATAOKA Y., TAMAOKI T., CHOE H.-R., TANAKA H., KATAOKA 1
PROC. NATL. ACAD. SCI. U.S.A. 86:5593-5697(1989).
-1- FUNCTION: PLAKS ESSENTIAL ROLES IN REGULATION CELLULAR
METABOLISM BY CATALYSING THE SYNTHESIS OF A SECOND MESSENGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRALM-S288C, A B972;
MEDLINE: 94378003.
JOHNSTON M., ANDREWS S., BRINKMAN R., COOPER J., DING H., DOVER
                                                                                                              -!- CATALYTIC ACTIVITY: ATP - 3',5'-CYCLIC AMP + PYROPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                          SYNTHESIS; MAGNESIUM
                                                                                                                                                                                                                                                                                                                                                                              LEUCINE-RICH REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20E7D7D8 CRC32;
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1. No. 4.88e+00;
Mismatches 3;
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EURARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1993 (REL. 27, CREATED)
01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
MITOCHONDRIAL 40S RIBOSOWAL PROTEIN MRP4.
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CATALYTIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 65;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                          CAMP
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MEDLINE; 92184810.
DAVIS S.C., TZAGOLOFF A., ELLIS S.
J. BIOL. CHEM. 267:5508-5514(1992)
[2]
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LRR
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57.1%;
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1692 AA;
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SACCHAROMYCES C
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ID RTO4_YEAST
AC P32902;
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VIRIDAE; DS-DNA NONENVELOPED VIRUSES; PAPOVAVIRIDAE; PAPILLOMAVIRUSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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(EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DELIGS H., TOPKANN B.;
CURR. TOP. MICROBIOL. IMMUNOL. 186:13-31(1994).
-!- FUNCTION: EZ IS A TRANSCRIPTIONAL TRANSACTIVATOR CAPABLE OF
ACTIVATIOR A CONDITIONAL ENHANCER IN THE VIRAL LONG CONTROL
REGION (LCR). EZ BINDS TO THE S'-ACCGNNNCGGT-3' PALINDROMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P11299; 2BOP.
EARLY PROTEIN; TRANSCRIPTION REGULATION; ACTIVATOR; DNA-BINDING;
TRANS-ACTING FACTOR.
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MEDILIE; 90046723.
YOUNG D., RIGGS M., FIELD J., VOJTEK A., BROEK D., WIGLER M.;
PROC. NATL. ACAD. SCI. U.S.A. 86:7989-7993(1989).
                                                                                                                                                                                                 Score 67; DB 1; Length 1477; Pred. No. 2.34e+00;
                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 66; DB 1; Length 461.
Pred. No. 3.39e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10; Indels
                                                                                                                                POTENTIAL.
W; 79B302B8 CRC32;
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EURARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52141 MW; DA2B4125 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-1994 (REL. 29, CREATED)
01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
01-CCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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                    POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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EMBL; X74464; G397073; -.
PIR; S36593; S36593.
                                                                                                                                                        MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P14605;
01-APR-1990 (REL. 14, CREATED)
01-APR-1990 (REL. 14, LAST SEQ
                                                                                                                                                                                                                                                                                      499 GRLQSLLEAPEDDPNQMIEM 518
                                                              759
799
1345
1366
1, 166727 1
                                                                                                                                                                                                                                                                                                             9 GRLQRLLQASGNHAAGILTM 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.7%;
38.5%;
                                                                                                                                                                                                   34.2%;
                                                                                                                                                                                                                       40.08;
                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 38.5%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGULATORY PROTEIN E2
                                                                                                                                                        Ą;
                                                                                                                                                                                                                   Best_Local Similarity
Matches 8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE; 94265501.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1996 (REL. ADENYLATE CYCLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [2]
SEQUENCE FROM N.A.
MEDLINE; 89345533.
                                                                                                                                                                                                                                                                                                                                                                                           LT 6
VE2_HPV09
P36780;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYAA_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYCLASE).
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Query Match

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KATTAL S.L., SINGH G., LOCKER J.L.;
AM. J. RESPIR. CELL MOL. BIOL. 6:446-452(1992).

-!- FUNCTION: IN PRESENCE OF CALCTUM IONS, PSAP BINDS TO SURFACTANT PHOSPHOLIPIDS AND CONTRIBUTES TO LOWER THE SURFACE TENSION AT THE ATR-LIQUID INTERFACE IN THE ALVEOLI OF THE MANMALIAN LUNG AND IS ESSENTIAL FOR NORMAL RESPIRATION.
-!- SUBBUNIT: OLICOMERIC COMPLEX OF 6 SET OF HOMOTRIMERS.
-!- FULMONARY SURFACTANT COMFISEN OF 90% LIPID AND 10% PROTEIN. THERE ARE 4 SURFACTANT ASSOCIATED PROTEIN: 2 COLLAGENOUS, CARBOHYDRATE-BINDING GLYCOPROTEINS (SP-A AND SP-D) AND 2 SMALL HYDROPHOBIC
                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PSO0615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
GLYCOPROTEIN; CALCIUM; SURFACE FILM; GASEOUS EXCHANGE; HYDROXYLATION; SIGNAL; LECTIN; COLLAGEN; REPEAT; POLYMORPHISM.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PULMONARY SURFACTANT PROTEIN A.
COLLAGEN-LIKE (WITH HYDROXYPROLINE).
C-TYPE LECTIN (SHORT FORM).
BY SIMILARITY.
BY SIMILARITY.
PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AGMENELLUM QUADRUPLICATUM)
                                                                                                                                                                                                    PROTEINS (SP-B AND SP-C).
SIMILARITY: CONTAINS A COLLAGENOUS DOMAIN.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
Li M13686; 1910670; -.
Li M30838; 6190655; -.
Li M68519; 6338049; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 90130334.
MURPHY R.C., GASPARICH G.E., BRYANT D.A., PORTER R.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 1.00e+01;
4; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . A (IN REF. 3).
R (IN G190565)
D (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P19737;
01-FEB-1991 (REL. 17, CREATED)
01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
HYPOTHEFICAL 28.7 KD PROTEIN IN RECA 37 REGION.
SYNEGROCOCOES SP. (STRAIN PCC 7002) (AGMENELLUM PROKARYOTA; GRACILICUTES; OXYPHOTOBACTERIA;
CYANOBACTERIA (BLUE-GREEN ALGAE); CHROOCOCCALES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               256 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ^ ^
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ^ ^
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32.1%;
similarity 56.3%;
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95 GPPGLPAHLDEELQAT 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 GPPGLQGRLQRLLQAS 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A24622; LNHUPS.
PIR; A25720; LNHUP6.
PIR; B25720; LNHUP1.
HSSP: P02462; IBBE.
MIM; 178630; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity
Matches 9; Conser
                 92198680
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P19737;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
                 MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                   EMBL; M3
EMBL; M6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
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                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSPA_HUMAN STANDARD; PRI; 248 AA.
907714;
01-APR-1998 (REL. 07, CREATED)
01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
901-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
901-MONARY SURFACTANT-ASSOCIATED PROFIEIN A PRECURSOR (SP-A) (PSP-A)
(PSAP) (ALVBOLAR PROTEINOSIS PROTEIN)
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE; 97070356.
MORRIS J.C., FINNERTY H., BENNET F., TURNER K.J., WOOD C.R.,;
EXP. HEMATOL. 24:1369-1376(1996).
-1- FUNCTION: TIES PROTEIN STIMULATES PLASMACYTOMA PROLIFERATION,
T-CELL-DEPENDENT DEVELOPMENT OF IMMUNGELOBULIN-PRODUCING B
CELLS AND SYNERGIZES WITH IL-3 IN SUPPORTING MURINE
MEGARARYCCYTE COLONY FORMATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [2]
SEQUENCE FROM N.A.
MEDLINE: 86014366.
WHITE R.T., DAMM D., MILLER J., SPRATT K., SCHILLING J., HAWGOOD BENSON B., CORDELL B.;
BENSON B., CORDELL B.;
[3]
                                                                                                                                                                                                                                                                                                                            EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
HELLONG: 86250832.
FLOROS J., STEINBRINK R., JACOBS K., PHELPS D., KRIZ R.,
FLOROS J., STEINBRINK R., JACOBS K., PHELPS D., KRIZ R.,
SULIZMAN L., JONES S., TAEUSCH H.W., FRANK H.A., FRITSCH
J. BIOL. CHEM. 261:9029-9033(1986).
                                                 Length 879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 199;
                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 63; DB 1; Len
Pred. No. 1.00e+01;
4; Mismatches 0;
                                              Score 64; DB 1; L
Pred. No. 7.01e+00;
   36 I -> L (IN REF. 3
96834 MW; 8BFD7CF3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 POTENTIAL.
199 INTERLEUKIN-11.
21522 MW; 1CB30772 CRC32;
                                                                                                                                                                                                                                    (REL. 33, CREATED)
(REL. 33, LAST SEQUENCE UPDATE)
(REL. 35, LAST ANNOTATION UPDATE)
                                                                              5; Mismatches
                                                                                                                                                                                                         199 AA
                                                                                                                                                                                                         PRT:
                                                                                                           GVDGRLQAILQAHENELGDFVLHM 419
                                                                                                                               6 GLQGRLQRLLQASGNHAAG-ILTM 28
                                                                                                                                                                                                                                                                                   INTERLEUKIN-11 PRECURSOR (IL-11)
                                              32.7%;
ilarity 45.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 32.1%;
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SFTPA OR SFTP1 OR PSAP
                                                                                                                                                                                                                                                                                                               MUS MUSCULUS (MOUSE).
                                 128 ALQARLERLIR 138
36
879 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAPIENS (HUMAN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              199 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 GLQGRLQRLLQ 16
                                                                                                                                                                                       LT 12
IL11_MOUSE
P47873;
01-FEB-1996 (
                                                                                                                                                                                                                                                      01-FEB-1996
 CONFLICT
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu Jul 30 09:12:01 1998; MasPar time 2.79 Seconds 251.630 Million cell updates/sec lar output not generated.

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Title:

>US-08-938-548A-4 (1-28) from US08938548A.pep 196 1 RSGPPGLOGRLOAGGNHAAGILIM 28 Description: Perfect Score: Sequence:

PAM 150 Gap 15 Scoring table:

69111 seqs, 25083644 residues Searched:

summaries Post-processing: Minimum Match 0% Listing first 45

swiss-prot35 1:swiss1 Database:

Mean 31.467; Variance 48.238; scale 0.652 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		œ	•				
Result	Score	Query Match	Length	DB	QI	Description	Pred. No.
	7.1	36.2	398	-	VE2_HPV63	REGULATORY PROTEIN E2.	5.14e-01
7	69	35.2	736	ч	ALD MOUSE	ADRENOLEUKODYSTROPHY P	1.11e+00
m	67	34.2	79	-	NIFU_FRAME	NIFU PROTEIN.	2.34e+00
4	67	34.2	442	-	HRDB_STRCO	RNA POLYMERASE PRINCIP	2.34e+00
'n	67	34.2	1477	Н	YOR1_YEAST	OLIGOMYCIN RESISTANCE	2.34e+00
Q	99	33.7	461		VE2_HPV09	REGULATORY PROTEIN E2.	3.39e+00
7	65	33.2	1692	ч	CYAA_SCHPO	ADENYLATE CYCLASE (EC	4.88e+00
۵	64	32.7	394	H	RT04_YEAST	MITOCHONDRIAL 40S RIBO	7.01e+00
0	64	32.7	400	H	ASSY_SYNY3	ARGININOSUCCINATE SYNT	7.01e+00
10	64	32.7	069	щ	VTER_EBV	PROBABLE DNA PACKAGING	7.01e+00
11	64	32.7	879	Н	YDBH_ECOLI	HYPOTHETICAL 96.8 KD P	7.01e+00
12	63	32.1	199	Н	IL11_MOUSE	INTERLEUKIN-11 PRECURS	1.00e+01
13	63	32.1	248	П	PSPA_HUMAN	PULMONARY SURFACTANT-A	1.00e+01
14	63	32.1	256	Н	YREC_SYNP2	HYPOTHETICAL 28.7 KD P	1.00e+01
15	63	32.1	324	ч	ANX3_RAT	ANNEXIN III (LIPOCORTI	1.00e+01
16	63	32.1	429	Н	UL88_HCMVA	PROTEIN UL88.	1.00e+01
17	63	32.1	878	П	ECR_DROME	ECDYSONE RECEPTOR (ECD	1.00e+01
18	63	32.1	972	-	POLS_IPNVJ	STRUCTURAL POLYPROTEIN	1.00e+01
19	63	32.1	1157	П	PEX1_PICPA	PEROXISOME BIOSYNTHESI	1.00e+01
20	63	32.1	1992	ч	TR12_HUMAN	THYROID RECEPTOR INTER	1.00e+01
21	62	31.6	187	Н	MT28_YEAST	TRANSCRIPTIONAL ACTIVA	1.43e + 01
22	62	31.6	511	Н	CTAQ_THEAQ	THERMOSTABLE CARBOXYPE	1.43e + 01
23	62	31.6	624	~1	SIR SYNP7	SULFITE REDUCTASE (FER	1.43e + 01

1.43e+01 1.43e+01	1.43e+01 1.43e+01	1.43e+01 1.43e+01	2.02e+01	2.02e+01	2.02e+01	2.02e+01	2.85e+01	2.85e+01	2.85e+01	2.85e+01	2.85e+01	2.85e+01	2.85e+01	2.85e+01	2.85e+01	2.85e+01	2.85e+01
GLYCOPROTEIN B PRECURS STRUCTURAL POLYPROTEIN	NITRITE REDUCTASE (NAD KINESIN-LIKE PROTEIN K	KINESIN-LIKE PROTEIN K FATTY ACID SYNTHASE (E	NEGATIVE FACTOR (F-PRO	MATING-TYPE LOCUS ALLE	HYPOTHETICAL 57.9 KD P	SERINE/THREONINE PROTE	SPORE MATURATION PROTE	INTERLEUKIN-11 PRECURS	OROTIDINE 5'-PHOSPHATE	HYPOTHETICAL 34.8 KD P	OUTER MEMBRANE PROTEIN	FACTOR VIII INTRON 22	PROBABLE ATP SYNTHASE	ALANINE AMINOTRANSFERA	ALANINE AMINOTRANSFERA	RNA POLYMERASE SIGMA F	HC-TOXIN SYNTHETASE (E
VGLB_MCMVS POLS_IPNVN	NIR_NEUCR KF1A_HUMAN	KF1A_MOUSE FAS_HUMAN	NEF_HV2NZ	B7_USTMA	YB77_YEAST	AFSK_STRCO	SPMB_BACSU	IL11_HUMAN	DCOP_MYCBO	YP95_CAEEL	YOPM_YERPE	F812_MOUSE	HRB6_XANCV	ALAT_HUMAN	ALAT_RAT	RPSD_CAUCR	HTS1_COCCA
дд,			П-	-	Н	7	-	Н	7	Н	-	-	Н	н	н	Н	н
928	1176	1695 2504	180	410	520	799	179	199	274	302	367	380	442	495	495	652	5217
31.6	31.6	31.6	31.1	31.1	31.1	31.1	30.6	30.6	30.6	30.6	30.6	30.6	30.6	30.6	30.6	30.6	30.6
622	62 62 63	62 62 63	19	61	61	61	9	9	9	9	9	9	9	9	9	9	9
25	26 27	7 7 8 7 8	30	35	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

									VIRIDAE; DS-DNA NONENVELOPED VIRUSES; PAPOVAVIRIDAE; PAPILLLOMAVIRUSES.				, DE VILLIERS E.M.;		-1- FUNCTION: E2 IS A TRANSCRIPTIONAL TRANSACTIVATOR CAPABLE OF	RAL LONG CONTROL	REGION (LCR). E2 BINDS TO THE 5'-ACCGNNNCGGT-3' PALINDROMIC					EARLY PROTEIN; TRANSCRIPTION REGULATION; ACTIVATOR; DNA-BINDING;			398.		4; Indels 0; Gaps 0	
	398 AA.			UPDATE)	N UPDATE)				; PAPOVAVIE				AWASHIMA M.		L TRANSACTI	R IN THE VI	-ACCGNNNCGC					ION; ACTIVA		CEO CRC32;	. ac	Pred. No. 5.14e-01:	4; Mismatches	
	PRT;		red)	SEQUENCE	ANNOTATIO			53.	ED VIRUSES				KURA I., K.		SCRIPTIONA	AL ENHANCE	TO THE 5'		A DIMER.			ON REGULAT	HORYLATION	MW; C9BBO	Score 71	Pred No	4; Misi	
	STANDARD;		(REL. 30, CREATED)	L. 30, LAST	L. 30, LAST	EIN E2.		VIRUS TYPE (NONENVELOP		i.A.	. 89	IS H., MATSUI	9-799(1993)	2 IS A TRAN	A CONDITION). E2 BINDS		NDS DNA AS 1	312096;	BOP.	TRANSCRIPTI(CTOR; PHOSPI	398 AA; 45450 MW; C9BB0CE0 CRC32;	36 28.	ity 55.68:	10; Conservative	
-	VE2_HPV63			01-0CT-1994 (RE		REGULATORY PROTEIN E2.		HUMAN PAPILLOMAVIRUS TYPE 63.	RIDAE; DS-DNA		SEQUENCE FROM N.A.	MEDLINE; 93276568.	AWA K., DELIU	ROLOGY 194:78	- FUNCTION: E	ACTIVATING	REGION (LCF	SEQUENCE.	-1- SUBUNIT: BINDS DNA AS A DIMER.	EMBL; X70828; G312096;	HSSP; P11299; 2BOP.	RLY PROTEIN;	TRANS-ACTING FACTOR; PHOSPHORYLATION.	SEQUENCE 398	Match Watch	Sect I macen. Best Local Similarity 55.68:	es 10; Cc	
RESULT 1		AC 007	DT 01	DT 01	DT 01	DE REC	GN E2	OS HU	OC VII	RN [1]	RP SE	RX MEI		RL VII		ខ		ខ	- ဗ		DR HS		KW TR	SQ SE	oi c	Rest	Matches	

295 RSPPKGGQSRLRRLIQEA 312 셤 à

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01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
ADRENOLEUKODYSTROPHY PROTEIN HOMOLOG (ALDP).
ALD OR ALDGH.
MUS MUSCULUS (MOUSE).
EUKRRYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MANMALIA;
EUTHERIA; RODENTIA. 736 AA. PRT; STANDARD; LT 2 ALD_MOUSE P48410; RESULT ROCOSEPTED

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the repeat lacking two cys residues. The same motif is found in albumin, vitamin D-binding protein and alpha-fetoprotein. The albumin, vitamin D-binding protein and alpha-fetoprotein. The disulphide-stabilized loop structure is thought to be conserved. The type II motif, related to repeats found in epidermal growth factor precursor is a 6-Cys pattern repeated nine times, although the ninth repeat in the A form is incomplete. Four of the repeats, (2, 3, 4 and 9) differ from the EGF-like motif in having a 4-6 residue insertion between cystelnes 4 and 5 instead of the usual single residue. Embodied within repeats 5, 6, 7 and 8 is the consensus sequence for Asp and Asn hydroxylation. The 7th repeat contains the consensus of glycosylation sequence, (XXXXC.)

Immediately following each repeat is a pentapeptide with the consensus sequence XD(IV)(D/N)E. Fibulin binds to the cytoplasmic domain of the betal submit of integrin adhesion receptors in a cation-dependent, EDTA-reversible manner. It can be used to manipulate adhesion of cells to fibronectin, collagen, laminin, and possibly also other proteins. Antibodies reactive with the protein have important diagnostic and therapeutic uses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 601; 5.91e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Beta-1 integrin; adhesion; receptor; fibronectin.
Homo saplens.
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/label- signal sequence
30..683
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Pred. No.
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16..69
label repeat unit 1
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..311
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R11150 standard; Protein; 683 AA.
811150;
21-MAY-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 10.1%;
Best Local Similarity 57.1%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= cm
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11D
 R1

12D
 R2

13D
 R3

14D
 R4

15D
 R5

15D

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Purified fibulin, DNA encoding it and antibodies reactive with it useful as diagnostic and therapeutic component.

- useful as diagnostic and therapeutic component.

Claim 10; Fig 5; 56pp; English.

The fibulin A, B and C forms are identical from their N-terminals to a divergence point at poss. 566 (terminal codon in fibulin A) after which they are distinct, encoding polypeptides of 566, 601 and 683 residues resp. All three forms are rich in cystelne (11 %) and analysis with no. and spacing of the Cys residues revealed two cypes of repeat moftif (I and II). The type I motif, CC(X)12C-(X)9-10C(X)6CC is repeated twice, separated by an imperfect form of the repeat lacking two Cys residues. The same motif is found in complement components C3a, C4a and C5a; the inverse is found in complement components C3a, C4a and C5a; the inverse is found in complement components C3a, C4a and C5a; the inverse is found in complement components C3a, C4a and C5a; the inverse is found in complement components C3a, C4a and C5a; the inverse is found in complement components C3a, C4a and C5a; the inverse is found in complement components C3a, C4a and C5a; the inverse is found in complement components C3a, C4a and C5a; the inverse is found in complement C5a; the think repeat in the A form is incomplete. Four of the repeats C5a; the ninth repeat in the A form is incomplete. Four of the repeat C5a; the ninth repeat in the A form is incomplete. Four of the cyco.

C5a, 3, 4 and 9) differ from the EGF-like motif in having a 4-6 consensus sequence C5a; propeats S, G, 7 and 8 is the consensus sequence C1App and Asn hydroxylation. The 7th repeat C5a contains the consensus O-1ycosylation sequence. CXCXC.

C6a Immediately following each repeats is a pentapeptide with the consensus Sequence C1AP) also other proteins and therapeutic uses.

C7 Immediately following each repeat is a pentapeptide with the protein have important diagnostic and therapeutic uses.

C8 also R11147, R11148 and R11149.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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26-APR-1991 (first entry)
Natural recombinant human lecithin:cholesterol acyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ä
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consensus pentapeptide
                                                                                                                                                                                                                                                                                     consensus pentapeptide
                                                                                                                                        'label consensus pentapeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= consensus pentapeptide
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480.484
// Tabel= re-
                                                                                                                                                   403.439
/label= repeat unit 6
                                                                  - repeat unit 5
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ID P70134 standard; Protein; 440 AA.
AC P70134;
T 26-APR-1991 (first entry)
DE Natural recombinant human lecithiu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-AUG-1990; U04662.
18-AUG-1989; US-395773.
(LJOL-) LA JOLLA CANCER RES.
(AMNA-) AMER NAT RED CROSS.
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WPI; 91-087250/12.
N-PSDB; Q11010.
                         ..397
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'label-
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ij

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New March 2012.

New multicistronic expression units - for producing equimolar march of polypeptide(s) in mammalian cells as hosts cards. of polypeptide(s) in mammalian cells as hosts

Claim 11; Page 29; 109pp; German.

A PDGF-AB heterodimer is recombinantly produced using a bicistronic expression unit in which a sequence responsible for internal translation start is located between cistrons coding for the PDGF-B and PDGF-A chains. The preferred PDGF-B sequence for inclusion in the bliststronic construct is 058725 which codes for the precursor sequence 241 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New vectors expressing platelet-derived growth factor B epitope(s) - and contg. c-sis or v-sis genes portions; are used to promote wound healing and produce antibodies

10 bisclosure: Fig 2, 49pp; English.

10 863469 describes the amino acid sequence of recombinant platelet derived growth factor B c-sis (rPDGF B c-sis). It may be used to promote wound healing, or as an antigen to prepare antisera or sequence 21 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-JUN-1995 (first entry)
Recombinant platelet derived growth factor B c-sis; rPDGF B c-sis; wound healing; antibody production.
                                                                                                                                                                                                                                                                                                                                                                                             /label= pre-peptide
82..190
/label= mature_PDGF-B
/note= "mature peptide is encoded by nucleotides
283-609 of Q58725"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 9.3%; Score 89; DB 9; Length 241; Local Similarity 43.6%; Pred. No. 1.94e+01; cs 17; Conservative 11; Mismatches 6; Indels
                                                                                                                                                 29-SEP-1994 (first entry)
Platelet-derived Growth Factor PDGF-B precursor.
Platelet-Derived Growth Factor; heterodimer; PDGF-AB;
recombinant protein production; PDGF-B chain;
bicistronic vector system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Achterberg V, Dirks W, Dorschner A, Eichner W, E
Meyer-Ingold W, Mielke H, Wirth M, Doerschner A;
WPI; 94-101190/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-AUG-1993; E02294.
27-AUG-1992; DE-228458.
(BEIE ) BEIERSDORF AG.
(GBEB ) GBF GES BIOTECH FORSCHUNG GMBH.
Achterberg V, Dirks W, Dorschner A,
                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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R63469 standard; protein; 241 AA.
                                                                                             standard; Protein; 241 AA
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Nicolson MA, Thomason AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EP-622456-A.
02-NOV-1994.
10-MAR-1988; 302116.
13-MAR-1997; US-025344.
19-FEB-1988; US-152045.
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                                                                                                                                                                                                                                                                                                               Homo sapiens.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                      with vector contg. new multi-cistronic expression unit, providing high level prodn. of pharmaceutical and cosmetic products Example 2.1.2; Page 23-24; 42pp; German. Pissmid phww-2 contains the cDNA of the human PDGF-B gene, but with the 5'-translated region of the precursor being incomplete (see Q80473; which encodes R68617). The BamHI/NcoI fragment of phww-2 was used as the basis for mutagenesis to isolate the sequence coding for mature PDGF-B with a Met residue at the N-terminus. The mutagenised coding sequence was used in the construction of multicistronic expression units for recombinant expression of the PDGF-A/B dimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Fig 4; 39pp; English.

Example 1 describes the subcloning and analysis of C-sis and V-sis genes encoding FDGFB chain.

Clone UZ-OS561 contains the c-sis gene encoding human PDGF B chain.

Exons 2-6 of this clone were subcloned and sequenced. They encode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                Recombinant multimeric protein prodn. in bacteria - transfected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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Pred. No. 1.94e+01;
11; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 89; DB 8; Length 220;
Pred. No. 1.94e+01;
11; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Monoclonal antibody; specific; epitope; B-Chain; PDGF; platelet-derived growth factor; wound healing; binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ||||||::: |: :| :| | | ::|:|||: :||||
79 LQRLLQAN-GNH-AAGI-LIMGR-RAGAELEPYPCPGRR 113
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                                                                                                                                                                             10-JUN-1993; 319708.
10-JUN-1993; DE-319708.
(BEIE) BELERSDORF AG.
(GBEB) GBF GES BIOTECH FORSCHUNG GMBH.
ELCHNET W. MCCARTHY JEG, Schneppe B; WPI; 95-023815/04.
N-PSDB; Q80473.
                                                                                             /label- mature_PDGF-B
/label= pre-region
/note= "truncated"
57..216
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R40965 standard; Protein; 220 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 43.6%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 9.3%;
Best Local Similarity 43.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-FEB-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thomason AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-SEP-1993.
10-MAR-1988; 302116.
13-MAR-1987; US-025344.
19-FEB-1988; US-152045.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93-282094/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              216 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AMGE-) AMGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
EP-559234-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in bacteria.
                                                                                                                            DE4319708-A
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Gaps

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Length 241;

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Disclosure, Fig 2, 788p; English, Sene chooling delive your process.

Herpes simplex virus-1 (CVG-2) was isolated from a recurrent facial cested and passaged a maximum of four times in cells in culture.

Viral DNA was prepd. from virons that accumulated in the cytoplasm of infected VERO cells (Kieff et al., J. Virol., 8, 125-132 (1971)).

CThe BamHI SP junction fragments contg. the domain of the gene that specified ICP34.5 were cloned into a puCIB plasmid using HSV-1(F) sequences as probes in colony blot hybridisation. Further subclonings were done to facilitate sequencing of different regions of the gene. HSV may be rendered avirulent by removing the ICP34.5 gene from the viral genome. The modified HSV genome is useful for preparing a stable, non-transforming live viral vaccine which cannot be catchivated from a latent state.

See also R21706,7.
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Pred. No. 2.30e+01;
4; Mismatches 1; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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The 4-1BB-L (ligand) protein is useful for exploring mechanisms of T-cell activation, as it is expressed on T lymphocytes. 4-1BB-L can be used as a tissue culture reagent for in vitro cultivation of primary T-cells during the derivation of clonal T-cell lines. It used in therapeutic procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T-cell; lymphocyte; activation; tissue culture; clone; cell lines; proliferation; stimulation; 4-1BB-L; ligand; receptor; cytokine.
deletion of ICP 34.5 gene encoding active gene prod.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 88; DB 4; Length 252;
Pred. No. 2.30e+01;
13; Mismatches 26; Indels
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R64190 standard; Protein; 254 AA.
R64190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-MAY-1994; UG5036.
07-MAY-1993; UG-060843.
(IMMY) IMMUNEX CORP.
Alderson MK, Goodwin RG, 5
WPI; 95-022265/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 9.2%;
Best Local Similarity 34.4%;
atches 22; Conservative
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Best Local Similarity 66.7%;
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human 4-1BB-L polypeptide
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127 GSRV 130
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